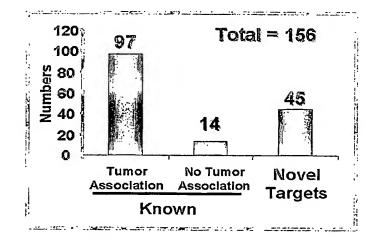


### 5 Figure 1. Advantage of Efficacy-First Discovery™ Method



10 Figure 2. Highly Enriched Tumor Targets

### siRNA-Mediated Target Validation (MDA-MB-435 Xenograft Model) 1400 P<0.01 N = 81200 Tumor Size (mm<sup>3</sup>) - ICTE1030-siRNA (Cell Surface Protein) -o--ICTB1031-siRNA (Ligand) - GFP-siRNA 800 P<0.05 400 10 24 27 **Days After Tumor Cell Inoculation**

Figure 3. Two Novel Targets Were Validated

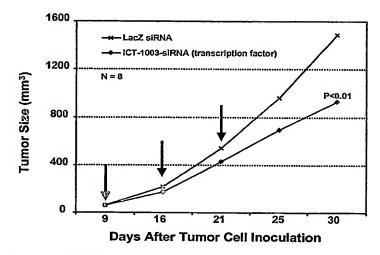


Figure 4. A Novel Targets Was Validated

5

# ICT1024, a growth factor receptor like protein

In vivo In vitro

# Apoptosis Activity Apoptosis Activity Induced by 1071-1024 sIRNA In ANDA-AIII-193 Cells See Street See See See See

# ICT-1024 siRNA mediated tumor growth inhibition in MDA-MB-435/nude mice model

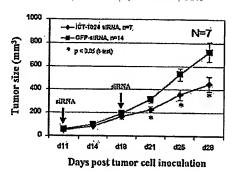


Figure 5.



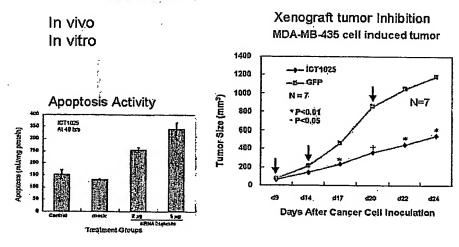
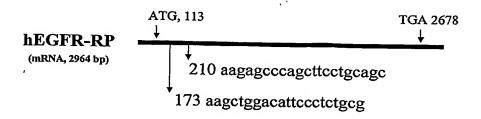


Figure 6.

5

Figure 7

ICT-1024 siRNA Design:



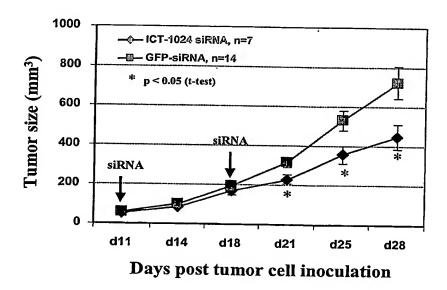


Figure 9.

Apoptosis Activity Induced by ICT-1024 siRNA
in MDA-MB-435 Cells

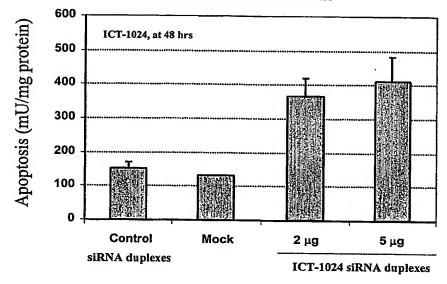


Figure 10. SAGE/Microarray Data

CGAP SAGE
Expression Data
and Correlation:
ICT1024 has
significantly
positive correlation
with other breast
cancer genes

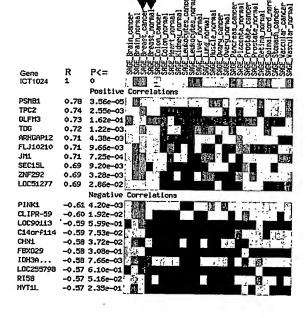
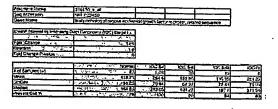
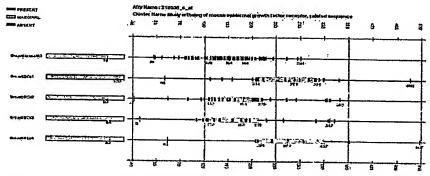


Figure 11 Cancer Tissue Distribution





ICT1024 is highly up regulated in all Stage I Breast Tumor samples (100%)

Figure 12. Consensus in rhomboid family

			10 20 30 40 50 60	
			* * * * *	
Human	consensus	1	PLOPGQLWRLITEMFLHAGILHLLFNMLSLLFFGIPLERRLGSVRFLLLYLLSGLAG- 57	,
Yeast	gi 9963865	99	ALRNWQVYRLVTYIFVYENPISLLCGAIIIWRFAGNFERTVGTVRHCFFTVIFAIFS- 15	55
Bacteria	gi 3738201	47	LLQKRQLYEIITYVTLHLSMLHIVFNFVSLLPAMSOFEKKOGTLACILVTVIPYTLPD 10	24
Yeast	gi 1653749	49	PRSLEGLRGIVFAPFLHADFGHLIANSVPFVVLAWLVMLO-EVSDFWIVTIITMVVG- 10	14
Human	gi 13621505	60	sksnarpvvaigdsdiysyriws-ffcqwintifcwsnrrplgltfflllyvlsgvwg- 11	17
Bacteria	gi 20139804	103	PEKREEAWRFISYMLVHAGVQHILGNLCMQLVLGIPLEMVHKGLRVGLVYLAGVIAG- 15	59
Human	gi 1169951	129	PTLKPEFWRYFTHALMHFSLMHILFNLLWWYLGGAVEKRLGSGKLIVIRSISALLS- 18	35
	gi 11066250	198	SNPASKVLCBPMLLSTPSHFSLFHMAANMYVLWSFSSSIVNILGGEOFMAVYLSAGVIS- 25	56
Bacteria	gi 13813618	68	yLVIKGYYSe-LFTSIFITNSFVDFIFNFISLYVIYLIFGSRAGKHEYGIFILAGILGN- 12	25
Plant	gi 9294149	242	I PKHKOLKRLFLSAFYHVNEPHLVYNMISLLWKGIKLETSMCSSEFASMVPTLIGMS- 29	8
			70 80 90 100 110 120	
Human			*	
	consensus	58	SLLSLLLSPASTPSVGASGAI FGLLGALLVILLPLNRILLLINPGAALFLLLGII 11	0
Yeası	gi 9963865	156	AIIPLSPEAVSsLSKLGEVEDARGPTPVAFAMLGVTTVRSRMRraLVFGMVVPSVL 21	1
Bacteria	gi 3738201	105	GIMHLIVYHFF1rkdyVSIAGLSGWAFAFISASCVHSPQRLISFFNLFSIPAYCF 15	9
Yeast	gi 1653749	105	GLGVWLIAPPNTVTVGASILIFGYLGFLLFRGWFQKNLASIV1-SIVVLVLYGSA 15	8
Human	gi 13621505	118	NAFTFWLTPETVAAGASTSLFGLFAAIVVLSFLGKNQALKD1-GKSYQTLIV-V 16	9
Bacteria	gi 20139804	160	SLASSIFDPLRYLVGASGGVYALMGGYFMNVLVNFQEMIPAFGIFRLLIIIL 21	1
Human	gi 1169951	186	GYVQQKFSGPWFGGLSGVVYALMGYVWLRGERDPQSGIYLQRGL1 23	0
Bacteria	gi 11066250	257	NFVSYLGKVATGIyGPSLGASGAIMTVLAAVCTKIPEGR-LAIIFLPMFTF 30	6
Plant	gl 13813618	126	LLTVIPYEPFTLSSGASGGIFGLLSYYTPYDFLKKDNLGVYGLVFLVSVF 17	5
Piant	gi 9294149	299	QGVTLLLAKSLLLLFDYDRAYYNEYAVGFSGVLFAMKVVLNSq-AEDYSSVYGIL 35	2
			130 140 150 160 170	
Human	consensus	111	······································	
Yeast	qi 9963865	212	LLNLLIGLLPGISNFGHLGGLLAGLLLGFILLRRPR 146	
Bacteria	gi 3738201	160	VPWLLLGABW11PQTSFLSNVCGLSIGLAYAHLLLFHRP 250	
	gi 1653749	159	PIIYLIMTtilVPKASFIGHASGAVMGYCTPFMLGSIPL 198	
Yeast	gi 13621505	170	LWGLLPGRAGVSWQGHLFGFIGGAIAAWLIAREKH 193	
Human -	91 20139804	212	NLIMNLFMPNVSMAGHIGGVVGGALLSIVFPTKMR 204	
Bacteria	gi 1169951	231	11VLDMGFALYRRFFVpedgsp-vsfaaHIAGGFAGMSIGYTVFSCFD 258	
Human	gi 11056250	307	IFALIWIVAGWFDLFGmsmangaHIAGLAVGLAMAFVDSLNAR 273	
Bacteria	gi 13813618	176	TAGNALKAIIAMDTAGmilgwkiidhaahlggalfgiwyvtygheliw 354	
Plant	g1 9294149	353	GVSDLIPPNVNVVAHIGGILGGIMYAVVYYLIRS 209	
	91 3234143	353	VPTKYAAWa-eLILVQMFVpnasflgHLGGILAGIIYLKLKGSYSG 397	

# Figure 13.

# Human rhomooid Proteins

# Human Rhomboid Family Protein Alignments

1 macourtdotablqrk/ppwikldipoxypicae-eps	0	13 Teach of the control of the contr		al iligakippomodoponin firsararekhasecovandregevqtaseeecsstlavvvkwpihpsap—elaghkrqfgavchqdprvodepseedpievpediikwpictknasgn dlihlgakispcirkdgqteqlvlrerdlerdagocvqndhagciqqrkdcaetlar rkwqddtgppmdkallgqktegavchqdprtceepsesgaliypddiikwpicreqaran algqfvlqvthpr algdsir-pokegdir-keinhv	Sed htmbphadovitgrpccigtkgrcoitarsycdfamgy(heeatlcaqubcoddvcg)l-pfl-npgvpdqfyrlwialf)hagilbcfvsicfqmtvjrdletlagwhriaifyllog 86 htmbphadovitgrpccigtigcesttroycefamgyfheeatlcaqubcoldvcgll-pfl-npgvbcaeartfamfvalatlsgrpwialfylagwhriaiftlag 87 de h-month and hagynghriaiftlag 88 htmbphadovitgrpccigtigcesttroycefamgyfheeatlcaqubcidvcgll-pfl-npgvbcaedyrvlalatlhagwhrivytwordqmtlrdlatlag 88 htmphagynghylagycoldfamgyfheeatlcaqubcidvcgll-pfl-npgvbcaedyrvlalatlhagwhrivytwordqmtlrdlatlag 88 htmphagynghylagycoldfamgyfheeatlcaqubcidvcgll-pfl-npgvbcaedyrvlalatlagwhrivytglyagylaeatlagwyagy 88 htmphylagycoldfamgyfyraglaeeaq	vçnləsənipyrasvypəgqqqqılacikvelfqə-vqılarpvrəffkilavvifitgqi-lpwi	788 pylafghtdlyrkroqilifquvEigllaglvvI£yvypyrcomcelltcipftdkfcekyeldaqlh
	20 118 68 234	12824		467 78 228 183 137 213	284 348 348 196 196	167 167 165 259 259 287	352 P S S S S S S S S S S S S S S S S S S
HRhombold 2 HRhombold 3 HRhombold 4 HRhombold 5 HRhombold 6 HRhombold 6 ICT-1024 HRhombold 3 HRhombold 6	HRhomboid 6 HRhomboid 5 HRhomboid 6 ICT-1024	HRhomboid 3 HRhomboid 4 HRhomboid 4 HRhomboid 5 HRhomboid 5	LCT-1024 HRhomboid 2 HRhomboid 3 HRhomboid 4 HRhomboid 5 HRhomboid 5	177-1024 HRhomboid 2 HRhomboid 3 HRhomboid 4 HRhomboid 5 HRhomboid 6	ICT-1024 HRhomboid 2 HRhomboid 3 HRhomboid 4 HRhomboid 5 HRhomboid 5	ICT-1024 MRhomboid 2 HRhomboid 3 HRhomboid 4 HRhomboid 5 HRhomboid 5	ICT-1024 HRhomboid 2 HRhomboid 3 HRhomboid 4 HRhomboid 5 HRhomboid 6

Figure 14. Function Domain Homology

ICT-1024, A Novel Member of Rhomboid Family

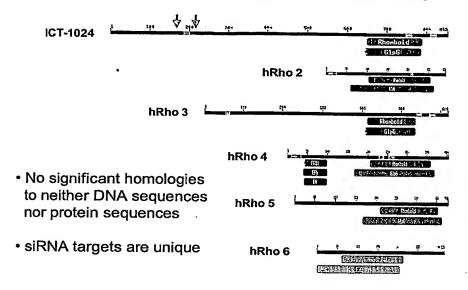
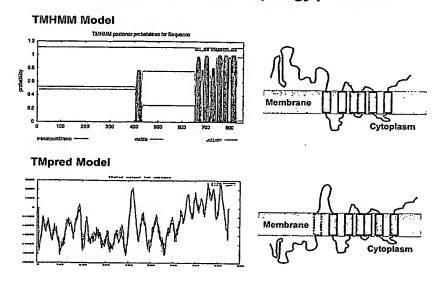


Figure 15. Hydrophobicity Analysis

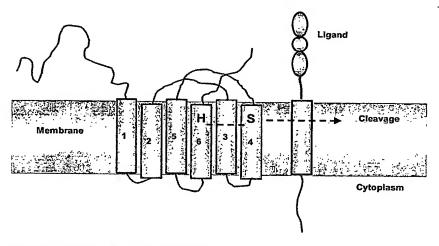
**Cellular Location and Topology predictions** 



# **Activation of EGFRs and ligands**

Figure 16.

## **ICT-1024 Intramembrane Protease Activity**



Refer to Koonin EV, et al. Genome Biology, 2003

Figure 17.

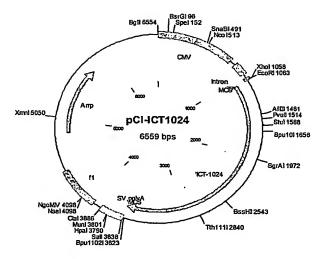


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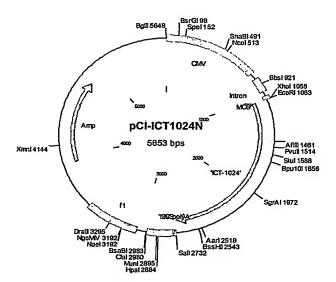


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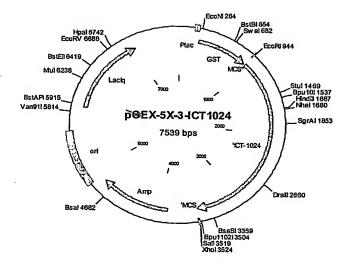


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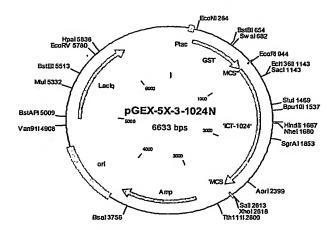


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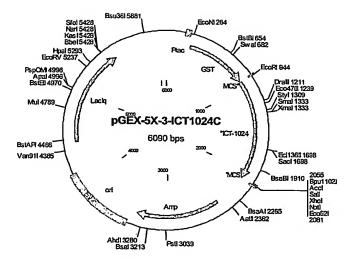


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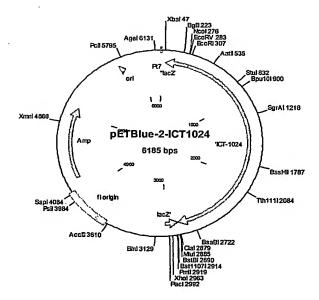


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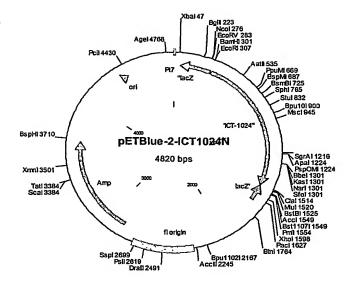


Figure 24

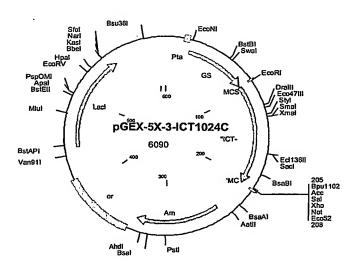


Fig. 25 (SEQ ID NO:58) ICT1024 PROTEIN (855 AA) CODING REGION: 1670-3637

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121	AATATGACCG	CCATGTTGGC	ATTGATTATT	AATATGACCG CCATGTTGGC ATTGATTATT GACTAGTTAT TAATAGTAAT CAATTACGGG	TAATAGTAAT	CAATTACGGG
181	GTCATTAGTT	CATAGCCCAT	ATATGGAGTT	CCGCGTTACA	CCGCGTIACA TAACTTACGG	TAAATGGCCC
241	GCCTGGCTGA		CCGCCCAACG ACCCCCCGCC		ATTGACGICA ATAATGACGI ATGTTCCCAT	ATGTTCCCAT
301	AGTAACGCCA	AGTAACGCCA ATAGGGACTT	TCCATTGACG	TCAATGGGTG	TCAATGGGTG GAGTATTTAC GGTAAACTGC	GGTAAACTGC
361	CCACTTGGCA	GTACATCAAG	TGTATCATAT	CCACTTGGCA GTACATCAAG TGTATCATAT GCCAAGTCCG CCCCCTATTG ACGTCAATGA	CCCCTATTG	ACGTCAATGA
421	CGGTAAATGG	CCCGCCIGGC	ATTATGCCCA	CGGTAAATGG CCCGCCTGGC ATTATGCCCA GTACATGACC TTACGGGACT TTCCTACTTG	TTACGGGACT	TTCCTACTTG
481	GCAGTACATC	TACGTATTAG	TCATCGCTAT	TACCATGGTG ATGCGGTTTT	ATGCGGTTTT	GGCAGTACAC
541	CAATGGGCGT	GGATAGCGGT	TTGACTCACG	TIGACICACG GGGAITICCA AGICICCACC CCAIIGACGI	AGTCTCCACC	CCATTGACGT
109	CAATGGGAGT		ACCAAAATCA	TIGITITGGC ACCAAAATCA ACGGGACTIT CCAAAAIGIC GTAATAACCC	CCAAAATGTC	GTAATAACCC
199	CGCCCGLIG	ACGCAAATGG	GCGGTAGGCG	CGCCCCGTTG ACGCAAATGG GCGGTAGGCG TGTACGGTGG GAGGTCTATA TAAGCAGAGC	GAGGTCTATA	TAAGCAGAGC
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901	ACTGGGCTTG	TCGAGACAGA	GAAGACTCTT	ACTGGGCTTG TCGAGACAGA GAAGACTCTT GCGTTTCTGA TAGGCACCTA	TAGGCACCTA	TTGGTCTTAC
961	TGACATCCAC	TTTGCCTTTC	TCTCCACAGG	TGTCCACTCC CAGTTCAATT		ACAGCTCTTA

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CTGGCGTGCC TICTTCAAGC TGCTGGCTGT GGTGCTCTTC CTCTTCACCT TTGGGCTGCT GCTGCCAGAT TCCTCTCTT CTGACAAGTT GCAGACATGA TAAGATACAT TGATGAGTTT GGACAAACCA CAACTAGAAT GCAGTGAAAA AATAAACAAG TTAACAACAA CAATTGCATT CATTTTATGT TTCAGGTTCA GGGGGAGATG CATCATCITT CAGGIGGICT ICCIGGGCCT CCIGGCIGGC CIGGIGGICC ICTICIACGI CTGTGAGAAG TACGAACTGG ACGCTCAGCT CCACTGAGTC GACCCGGGCG GCCGCTTCGA AAATGCTTTA TTTGTGAAAT TTGTGATGCT ATTGCTTTAT TTGTAACCAT TATAAGCTGC TITIAAAGCAA GIAAAACCIC IACAAAIGIG GIAAAAICGA IAAGGAICCG GGCIGGCGIA AIAGCGAAGA GGCCCGCACC GAICGCCCII CCCAACAGII GCGCAGCCIG AATGGCGAAT GGACGCGCC TGTAGCGGCG CATTAAGCGC GGCGGGTGTG GTGGTTACGC CCITICICGC CACGIICGCC GGCIIIICCCC GICAAGCICI AAAICGGGGG CICCCIIIAG GCAGCGTGAC CGCTACACTT GCCAGCGCCC TAGCGCCCGC TCCTTCGCT TTCTTCCCTT GGTTCCGATT TAGAGCTTTA CGGCACCTCG ACCGCAAAAA ACTTGATTTG GGTGATGGTT CACGIAGIGG GCCAICGCCC IGAIAGACGG ITTITCGCCC ITIGACGIIG GAGICCACGI TCTTTAATAG TGGACTCTTG TTCCAAACTG GAACAACACT CAACCCTATC TCGGTCTATT CTTTTGATTT ATAAGGGATT TTGCCGATTT CGGCCTATTG GTTAAAAAT GAGCTGATTT AACAAATATT TAACGCGAAT TTTAACAAA TATTAACGTT TACAATTTCG CCTGATGCGG GCCGTGGATT GACAACTTTG CCCACATCTC GGGGTTCATC AGTGGCCTCT CGCCTTCTTG CCCTACATCA GCTTTGGCAA GTTCGACCTG TACCGGAAAC CTAICCIGIC CGCIGIGAGI GGIGIGAGII CCICACCIGC AICCCCIICA TGGGAGGTTT 3301 3361 3421 3481 3541 3601 3661 3721 3781 3841 3901 3961 4021 4081 4141 4201 4261 4321 438I

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4681	GTGATACGCC	TATTTTATA	GGTTAATGTC	ATGATAATAA	TGGTTTCTTA	GACGTCAGGT
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5401	ACGATGCCTG	TAGCAATGGC	AACAACGITG	CGCAAACTAT	TAACTGGCGA	ACTACTTACT
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GCGGAGCCTA	TTGTGATGCT CGTCAGGGGG GCGGAGCCTA		GCGTCGATTT	TTTCGCCACC TCTGACTTGA GCGTCGATTT	TTTCGCCACC	6421
rccrercess	GGAGAGCGCA CGAGGGAGCT TCCAGGGGGA AACGCCTGGT ATCTTTATAG TCCTGTCGGG	AACGCCTGGT	TCCAGGGGA	CGAGGGAGCT	GGAGAGCGCA	6361
GGTCGGAACA	AAAGGCGGAC AGGTATCCGG TAAGCGGCAG	AGGTATCCGG	AAAGGCGGAC	CCGAAGGGAG	GCCACGCTTC	6301
ATGAGAAAGC	AGATACCTAC AGCGTGAGCT ATGAGAAAGC	AGATACCTAC	CACCGAACTG	AGCTTGGAGC GAACGACCTA CACCGAACTG	AGCTTGGAGC	6241
CACACAGCCC	CGGATAAGGC GCAGCGGTCG GGCTGAACGG GGGGTTCGTG CACACAGCCC	GGCTGAACGG	GCAGCGGTCG	CGGATAAGGC	CGATAGTTAC	6181
GGACTCAAGA	TTACCGGGTT	AAGTCGTGTC	CAGTGGCGAT	TGGCTGCTGC	CTGTTACCAG	6121
TCTGCTAATC	CATACCTCGC	GCACCGCCTA	ACCACTICAA GAACTCTGIA	ACCACTICAA	TAGTTAGGCC	6061
AGTGTAGCCG	ATACCAAATA CTGTCCTTCT AGTGTAGCCG		CAGAGCGCAG	CCGAAGGTAA CTGGCTTCAG CAGAGCGCAG	CCGAAGGTAA	6001
AACTCTTTT	ITGCCGGAIC AAGAGCIACC AACICITITI		GGTGGTTTGT	AAAAAACCAC CGCTACCAGC GGTGGTTTGT	AAAAAACCAC	5941
CTTGCAAACA	TAATCTGCTG	TTTCTGCGCG	AGATCCTTTT	GATCTTCTTG	AAGATCAAAG	5881
CCCCGTAGAA	GAGCGTCAGA CCCCGTAGAA	TCGTTCCACT	ACGIGAGIII	AAATCCCTTA	CTCATGACCA	5821
TTTGATAAT	TGAAGAICCI TTTTGATAAI	TTAATTTAAA AGGATCTAGG		ATTGATTTAA AACTTCATTT	ATTGATTTAA	5761
TATACTTTAG	TTTACTCATA	TCAGACCAAG	TTGGTAACTG	TGATTAAGCA	GGTGCCTCAC	5701
CGCTGAGATA	ATAGACAGAT	GATGAACGAA	CGGGGAGTCA GGCAACTATG	CGGGGAGTCA	ATCTACACGA	5641
TATCGTAGIT	GGGTCTCGCG GTATCATTGC AGCACTGGGG CCAGATGGTA AGCCCTCCCG TATCGTAGTT	CCAGATGGTA	AGCACTGGGG	GTATCATTGC	GGGTCTCGCG	5581

26 (SEQ ID NO:60) ICT1024 N TERMINUS 553 AA CODING REGION: 1070-2731

TCAATATTGG CCATTAGCCA TATTATTCAT TGGTTATATA GCATAAATCA ATATTGGCTA TIGGCCATIG CAIACGIIGI AICIAIAICA IAAIAIGIAC AITIAIAIIG GCICAIGICC CAATTACGGG GTCATTAGTT CATAGCCCAT ATATGGAGTT CCGCGTTACA TAACTTACG TAAATGGCCC AGTAACGCCA ATAGGGACTT TCCATTGACG TCAATGGGTG GAGTATTTAC GGTAAACTGC GCCIGGCTGA CCGCCCAACG ACCCCCGCCC ATTGACGTCA ATAATGACGT ATGTTCCCAT CGGTAAATGG CCCGCCTGGC ATTATGCCCA GTACATGACC TTACGGGACT TTCCTACTTG GCAGTACATC TACGTATTAG TCATCGCTAT TACCATGGTG ATGCGGTTTT GGCAGTACAC CAATGGGAGT TIGITITGGC ACCAAAATCA ACGGGACTIT CCAAAAIGIC GIAATAACCC CGCCCCGTIG ACGCAAAIGG GCGGTAGGCG IGTACGGTGG GAGGICTAIA TAAGCAGAGC CCACTIGGCA GTACATCAAG IGTAICATAI GCCAAGICCG CCCCCIAIIG ACGICAAIGA CAATGGGCGT GGATAGCGGT TTGACTCACG GGGATTTCCA AGTCTCCACC CCATTGACGT TCGTTTAGTG AACCGTCAGA TCACTAGAAG CTTTATTGCG GTAGTTTATC ACAGTTAAAT TGCTAACGCA GTCAGTGCTT CTGACAAC AGTCTCGAAC TTAAGCTGCA GAAGTTGGTC ACTGGGCTTG TCGAGACAGA GAAGACTCTT GCGTTTCTGA TAGGCACCTA TTGGTCTTAC TGACATCCAC TTTGCCTTTC TCTCCACAGG TGTCCACTCC CAGTTCAATT ACAGCTCTTA GTGAGGCACT GGGCAGGTAA GTATCAAGGT TACAAGACAG GTTTAAGGAG ACCAATAGAA AATAIGACCG CCAIGTIGGC ATIGATIAIT GACTAGTIAI IAATAGTAAI 121 61 181 241 301 361 421 541 721 781 481 601 199 841 901 196

	GCAAGCTCTT	GGIGAGCACC GCGGGGCCGC GACGGGCCA GCGIAICGCG GIGCCGGIGC GCAAGCICII	GCGTATCGCG	GACGGGGCCA	ටපටටපපටපටප	GGTGAGCACC	2101
	GACAGGAGGT	GTGCGGCTCC	CCGCAGCCCC GCAGCCCAAG		AAGGAGGCG	GCGGAAGCAG	2041
	AGCGAGGCTG	CIGCCCIIGG	CCACCTGATG	TTGAGCGCAG	CGCAGCGAGC	GGCCCTGGAC	1981
•	TCACCGGCGG	CAGGCGGACC	ACTGGGAGAA GGCACCGGAG		GCGCTAAAGG	ATCGGAGGCA	1921
	TCGAGTCCCC	GATGAAGTTT	CACATACCCG	AAGAGCTGTC	ATCCTCCATG	CCGGGAAGGT	1861
	CCTTCTTGC	CTGGACACAT	CCCCGATGAG	CAACTGATTT	GAGGAGGACA	TAGCTTTCTG	1801
	TCACTCCAGC	CGTCGAAGCT	CCGGGCACGG	GCACCTTTCG	GTTAGGGATG	AGGCCGCTCC	1741
	CGCTGATGAA	GCGCCCCAG	GAGCTTCCGG	TGGCCAAGAT	CGAGAGTCGG	GCGGCGCAAG	1681
	GGCTCCCGCG	GGTTTCCACC	CTCCCGCTCA	CCTTCTCCAG	TCCCTCTGCT	GGGTGCTGCC	1621
	CCGTCACGCC	CCACACACTC	CCTGAGTGCC	CTGCGGAAGG	GCAGATGACA	CTTCCGTGTG	1561
	GTGGCCGTGC	CCCCTGGCCC	GATCATAGAC	GCATGCAGAA	TGCCAGCTGG	CGTGGGGCCA	1501
	CCCCACTCTA	GAGACGCCAC	GACCAGCACC	ACGIGICGCI	AGCCAGGACA	GGACCTGCCC	1441
	TCCGGGAGCT	CCCCAGGICC	GAAGCTGAAG	AGCGCTACGG	CACTGCAGCC	GAGCATCCGT	1381
	GGCAGCGCAA	ACCCAGAAAT	CAGTGACAGC	TGAGCAAGGA	TGGTTTGGAG	GACCGCCGAC	1321
	TCCGCAGGGG	ACACAGACCA	GACGICCAIC	TGCAACGCCA	ದರತಿದ್ದಾರವಾ	TGAGCTCCGG	1261
	CACCCCACCA	CACATCTCTT	CGAGACAGCC	GTATGCCAGC	AGGAGTGTGA	GGCTTTCCTG	1201
	TGAGGCGACA	CTGCAGCCCC	GCCCAGCTTC	CGGCAGAAGA	GTGCCCCTGA	TCCCTCTGCG	1141
	AGCTGGACAT	CCCTGGCTAA	CAAGAAGCCA	GCCTGCAGCG	AGCACGAGCA	CCGCAGGGAC	1081
	TGAGTGAGGC	AGGCTAGAGT ACTTAATACG ACTCACTATA GGCTAGCCTC GAGAATTCCA TGAGTGAGGC	GGCTAGCCTC	ACTCACTATA	ACTTAATACG	AGGCTAGAGT	1021

CGCCCGGGAG AAGCGGCCGT ATGGGCTGGG CATGGTGGGA CGGCTCACCA ACCGCACCTA CCGCAAGCGC ATCGACAGCT TCGTCAAGCG CCAGATCGAG GACATGGACG ACCACAGGCC CITCITCACC TACTGGCTTA CCTTCGTGCA CTCGCTCGTC ACCATCCTAG CCGTGTGCAT TGCTGCGGAA CCGCGGGGTC TACGAGAACG TCAAGTACGT GCAGCAGGAG AACTTCTGGA TCGGGCCCAG CTCGGAGGCC CTCATCCACC TGGGCGCCAA GTTTTCGCCC TGCATGCGCC AGGACCCGCA GGTGCACAGC TTCATTCGCT CGGCGCGCAA GCGCGAGAAG CACTCCGCCT GCTGCGTGCG CAACGACAGG TCGGGCTGCG TGCAGACCTC GGAGGAGGAG TGCTCGTCCA CGCTGGCAGT GTGGGTGAAG TGGCCCATCC ATCCCAGCGC CCCAGAGCTT GCGGGCCACA AGAGACAGTT TGGCTCTGTC TGCCACCAGG ATCCCAGGTG AGTCGACCCG GGCGGCCGCT TCGAGCAGAC ATGATAAGAT ACATTGATGA GTTTGGACAA ACCACAACTA GAATGCAGTG AAAAAAATGC TITAITIGIG AAAITIGIGA IGCIAIIGCI ITAITIGIAA CCAITAIAAG CIGCAAIAAA CAAGITAACA ACAACAATIG CAITCAITIT AIGITITCAGG ITCAGGGGGA GAIGIGGGAG GTTTTTAAA GCAAGTAAAA CCTCTACAAA TGTGGTAAAA TCGATAAGGA TCCGGGCTGG CGTAATAGCG AAGAGGCCCG CACCGATCGC CCTTCCCAAC AGTTGCGCAG CCTGAATGGC GAATGGACGC GCCCTGTAGC GGCGCATTAA GCGCGGGGGG TGTGGTGGTT ACGCGCAGCG TCGCCACGIT CGCCGGCTTT CCCCGTCAAG CTCTAAATCG GGGGCTCCCT TTAGGGTTCC GATITIAGAGC TITIACGGCAC CICCACCGCA AAAAACTIGA ITIGGGIGAI GGIICACGIA IGACCGCIAC ACTIGCCAGC GCCCIAGCGC CCGCICCIII CGCIIITCIIC CCIICCIIIC CTAIGGCAIC GCGCCCGIGG GCIICICGCA GCAIGAGACG GIGGACICGG 2161 2221 2341 2281 2401 2461 2521 2581 2641 2881 2941 3001 2701 2761 2821 3061 3121 3181 3241

GIGGCCCAIC GCCCIGAIAG ACGCITITIC GCCCITIGAC GIIGGAGICC ACGIICTITA CITGITCCAA ACTGGAACAA CACTCAACCC TATCTCGGTC TATCTTTTG ATTIATAAGG GATTITGCCG ATTICGGCCT ATTGGTTAAA AAATGAGCTG ATTIAACAAA TACAATCTGC CGGGCTTGTC TGCTCCCGGC ATCCGCTTAC AGACAAGCTG TGACCGTCTC CGGGAGCTGC TATITIAACGC GAATITITAAC AAAATAITIAA CGITITACAAI TICGCCIGAI GCGGIAITITI ICIGAIGCCG CAIAGITAAG CCAGCCCCGA CACCCGCCAA CACCCGCTGA CGCGCCCTGA ATGIGICAGA GGITITCACC GICAICACCG AAACGCGCGA GACGAAAGGG CCICGIGAIA GTTTTTGCTC ACCCAGAAAC GCTGGTGAAA GTAAAAGATG CTGAAGATCA GTTGGGTGCA CGAGTGGGTT ACATCGAACT GGATCTCAAC AGCGGTAAGA TCCTTGAGAG TTTTCGCCCC GAAGAACGIT ITCCAAIGAI GAGCACITIT AAAGIICIGC IAIGIGGCGC GGIAITAICC GAATGACTTG CGCCTATITI IAIAGGITAA IGTCAIGAIA ATAAIGGIII CITAGACGIC AGGIGGCACI TTTCGGGGAA ATGTGCGCGG AACCCCTATT TGTTTATTTT TCTÁAATACA TTCAAATATG TATCCGCTCA TGAGACAATA ACCCTGATAA ATGCTTCAAT AATATTGAAA AAGGAAGAGT TIGCCITCCI GTIGAGTACT CACCAGICAC AGAAAAGCAI CITACGGAIG GCAIGACAGI AAGAGAATIA IGCAGTGCTG CCATAACCAT GAGTGATAAC ACTGCGGCCA ACTTACTTCT GACAACGATC GGAGGACCGA AGGAGCTAAC CGCTTTTTG CACAACATGG GGGATCATGT AACTCGCCTT CICCTIACGC AICIGIGCGG TATITICACAC CGCATAIGGI GCACICICAG ATGAGTATIC AACATIICCG IGICGCCCII AITCCCTIII IIGCGGCAII CGTATTGACG CCGGGCAAGA GCAACTCGGT CGCCGCATAC ACTATTCTCA ATAGTGGACT 3301 3421 3481 3541 3601 3721 3841 4141 4261 4381 3661 3781 3901 3961 4201 4321 4021 4081

GATCGTTGGG AACCGGAGCT GAATGAAGCC ATACCAAACG ACGAGCGTGA CACCACGATG CCTGTAGCAA TGGCAACAAC GTTGCGCAAA CTATTAACTG GCGAACTACT TACTCTAGCT CGCGGTATCA TIGCAGCACT GGGCCCAGAI GGIAAGCCCI CCCGIAICGI AGIIAICIAC TCCCGGCAAC AATTAATAGA CTGGATGGAG GCGGATAAAG TTGCAGGACC ACTTCTGCGC TCGGCCCTTC CGGCTGGCTG GTTTATTGCT GATAAATCTG GAGCCGGTGA GCGTGGGTCT TTAGATTGAT ACGACGGGGA GTCAGGCAAC TATGGATGAA CGAAATAGAC AGATCGCTGA GATAGGTGCC TAATCTCATG ACCAAAATCC CTTAACGTGA GTTTTCGTTC CACTGAGCGT CAGACCCCGT AGAAAAAGATC AAAGGATCTT CTTGAGATCC TTTTTTTCTG CGCGTAATCT GCTGCTTGCA AACAAAAAA CCACCGCTAC CAGCGGTGGT TTGTTTGCCG GATCAAGAGC TACCAACTCT TTTTCCGAAG GTAACTGGCT TCAGCAGAGC GCAGATACCA AATACTGTCC TTCTAGTGTA GCCGTAGTTA CCAGIGGCIG CIGCCAGIGG CGAIAAGICG IGICTIACCG GGIIGGACIC AAGACGAIAG GGCCACCACT ICAAGAACTC IGTAGCACCG CCTACATACC ICGCICTGCT AAICCIGITA TTACCGGATA AGGCGCAGCG GTCGGGCTGA ACGGGGGGTT CGTGCACACA GCCCAGCTTG GAGCGAACGA CCTACACCGA ACTGAGATAC CTACAGCGTG AGCTATGAGA AAGCGCCACG CTTCCCGAAG GGAGAAAGGC GGACAGGTAT CCGGTAAGCG GCAGGGTCGG AACAGGAGAG CGCACGAGGG AGCTTCCAGG GGGAAACGCC TGGTATCTTT ATAGTCCTGT CGGGTTTCGC CACCICIGAC TIGAGCGICG ATTITIGIGA IGCICGICAG GGGGGCGGAG CCIAIGGAAA CATATATACT TIAAAACTIC AITITIAAII IAAAAGGAIC IAGGIGAAGA ICCIIITIGA TCACTGATTA AGCATTGGTA ACTGTCAGAC CAAGTTTACT 4441 4501 4561 4621 4681 4741 4801 4861 4921 4981 5041 5161 5221 5401 5281 5341

5581 AACGCCAGCA ACGCGGCCTT TTTACGGTTC CTGGCCTTTT GCTGGCCTTT TGCTCACATG

5641 GCTCGACAGA TCT

Fig. 27, (SEQ ID NO: 61) ICT1024 coding region: 947-3518

Н	TCGACTCGAG	TCGACTCGAG CGGCCGCATC	GTGACTGACT	GACGATCTGC	CTCGCGCGTT	GTGACTGACT GACGATCTGC CTCGCGCGTT TCGGTGATGA
19	CGGTGAAAAC		CICTGACACA TGCAGCTCCC GGAGACGGTC ACAGCTTGTC	GGAGACGGTC	ACAGCTTGTC	TGTAAGCGGA
121		TGCCGGGAGC AGACAAGCCC GTCAGGGCGC GTCAGCGGGT	GTCAGGGCGC	GTCAGCGGGT	GTTGGCGGGT	GTCGGGGCGC
181	AGCCATGACC	AGCCATGACC CAGTCACGTA GCGATAGCGG	GCGATAGCGG	AGTGTATAAT	TCTTGAAGAC	GAAAGGGCCT
241	CGTGATACGC	CIATTTTAT	AGGTTAATGT		CATGATAATA ATGGTTTCTT	AGACGICAGG
301	TGGCACTTTT		CGGGGAAATG TGCGCGGAAC	CCCTATTIGT	TTATTTTCT	AAATACATTC
361	AAATATGTAT	CCGCTCATGA	CCGCTCATGA GACAATAACC CTGATAAATG	CTGATAAATG	CTTCAATAAT	ATTGAAAAG
421	GAAGAGTATG	AGTATTCAAC	ATTTCCGTGT	CGCCCTTAIT	CCCTTTTTG	CGGCATTTTG
481	· CCTTCCTGTT		TTTGCTCACC CAGAAACGCT	GGTGAAAGTA	GGTGAAAGTA AAAGATGCTG AAGATCAGTT	AAGATCAGTT
541	GGGTGCACGA	GGGTGCACGA GTGGGTTACA	TCGAACTGGA	TCTCAACAGC	TCGAACTGGA TCTCAACAGC GGTAAGATCC TTGAGAGTTT	TTGAGAGTTT
601	TCGCCCCGAA	TCGCCCCGAA GAACGITITC CAAIGAIGAG		CACTTTTAAA	CACTITIAAA GIICIGCIAI	GTGGCGCGGT
661	ATTATCCCGT	ATTATCCCGT GTTGACGCCG	GGCAAGAGCA ACTCGGTCGC	ACTCGGTCGC	CGCATACACT	ATTCTCAGAA
721	TGACTTGGTT	GAGTACTCAC	CAGTCACAGA AAAGCATCTT ACGGATGGCA	AAAGCATCTT	ACGGATGGCA	TGACAGTAAG
781	AGAATTATGC	AGAATTATGC AGTGCTGCCA	TAACCATGAG	TGATAACACT	TGATAACACT GCGGCCAACT TACTTCTGAC	TACTTCTGAC
841	AACGATCGGA	AACGATCGGA GGACCGAAGG AGCTAACCGC		TTTTTTGCAC AACATGGGGG		ATCATGTAAC
901	TCGCCTTGAT	CGTTGGGAAC	CGGAGCTGAA	TGAAGCCATA	CCAAACGACG	AGCGTGACAC
196	CACGATGCCT	CACGATGCCT GCAGCAATGG CAACAACGTT GCGCAAACTA TTAACTGGCG AACTACTTAC	CAACAACGIT	GCGCAAACTA	TTAACTGGCG	AACTACTTAC

TCTAGCTTCC CGGCAACAAT TAATAGACTG GATGGAGGCG GATAAAGTTG CAGGACCACT TCTGCGCTCG GCCCTTCCGG CTGGCTGGTT TATTGCTGAT AAATCTGGAG CCGGTGAGCG TGGGTCTCGC GGTATCATTG CAGCACTGGG GCCAGATGGT AAGCCCTCCC GTATCGTAGT TATCTACACG ACGGGGAGTC AGGCAACTAT GGATGAACGA AATAGACAGA TCGCTGAGAT AGGIGCCICA CIGATIAAGC ATIGGIAACI GICAGACCAA GITIACICAI AIAIACITIA GATTGATTTA AAACTTCATT TTTAATTTAA AAGGATCTAG GTGAAGATCC TTTTTGATAA TCTCATGACC AAAATCCCTT AACGIGAGTT TTCGTTCCAC TGAGCGTCAG ACCCCGTAGA AAAGATCAAA GGATCTTCTT GAGATCCTTT TTTTCTGCGC GTAATCTGCT GCTTGCAAAC AAAAAAACCA CCGCTACCAG CGGTGGTTTG TTTGCCGGAT CAAGAGCTAC CAACTCTTTT TCCGAAGGTA ACTGGCTTCA GCAGAGCGCA GATACCAAAT ACTGTCCTTC TAGTGTAGCC GTAGTTAGGC CACCACTTCA AGAACTCTGT AGCACCGCCT ACATACCTCG CTCTGCTAAT CCIGITACCA GIGGCIGCIG CCAGIGGCGA TAAGICGIGI CTIACCGGGI IGGACICAAG ACGATAGTTA CCGGATAAGG CGCAGCGGTC GGGCTGAACG GGGGGTTCGT GCACAGCC CAGCITGGAG CGAACGACCI ACACCGAACI GAGAIACCIA CAGCGIGAGC IAIGAGAAAG CGCCACGCTT CCCGAAGGGA GAAAGGCGGA CAGGTATCCG GTAAGCGGCA GGGTCGGAAC AGGAGAGCGC ACGAGGGAGC TTCCAGGGGG AAACGCCTGG TATCTTTATA GTCCTGTCGG ATGGAAAAAC GCCAGCAACG CGGCCTTTTT ACGGTTCCTG GCCTTTTGCT GGCCTTTTGC GGCGGAGCCT TCACATGTTC TTTCCTGCGT TATCCCCTGA TTCTGTGGAT AACCGTATTA CCGCCTTTGA GITICGCCAC CICTGACTIG AGCGICGAIT TITGIGATGC ICGICAGGGG 1081 1201 1141 1261 1321 1381 1441 1501 1561 1621 1741 1681 1861 1981 2041 2101

GTGAGCTGAT ACCGCTCGCC GCAGCCGAAC GACCGAGCGC AGCGAGTCAG TGAGCGAGGA AGCGGAAGAG CGCCTGATGC GGTATTTTCT CCTTACGCAT CTGTGCGGTA TTTCACACCG CATAAATTCC GACACCATCG AATGGTGCAA AACCTTTCGC GGTATGGCAT GATAGCGCCC GGAAGAGAGT CAATTCAGGG TGGTGAATGT GAAACCAGTA ACGTTATACG ATGTCGCAGA GCCACGTTTC TGCGAAAACG CGGGAAAAG TGGAAGCGGC GATGGCGGAG CTGAATTACA TTCCCAACCG CGTGGCACAA CAACTGGCGG GCAAACAGTC GTTGCTGATT GGCGTTGCCA CCTCCAGTCT GGCCCTGCAC GCGCCGTCGC AAATTGTCGC GGCGATTAAA TCTCGCGCCG ATCAACTGGG TGCCAGCGTG GTGGTGGA TGGTAGAACG AAGCGGCGTC GAAGCCTGTA AAGCGGCGGT GCACAAICII CICGCGCAAC GCGICAGIGG GCIGAICAII AACIAICCGC IGGAIGACCA GGAIGCCAIT GCIGIGGAAG CIGCCIGCAC IAAIGIICCG GCGIIAIIIC IIGAIGICIC TGACCAGACA CCCATCAACA GTATTATTTT CTCCCATGAA GACGGTACGC GACTGGGCGT GGAGCAICTG GICGCAITGG GICACCAGCA AAICGCGCTG IIAGCGGGCC CAITAAGIIC TGTCTCGGCG CGTCTGCGTC TGGCTGGCTG GCATAATAT CTCACTCGCA ATCAAATTCA GCCGATAGCG GAACGGGAAG GCGACTGGAG TGCCATGTCC GGTTTTCAAC AAACCATGCA GCCAACGATC AGATGGCGCT GGGCGCAAIG CGCGCCAITA CCGAGICCGG GCIGCGCGIT GGIGCGGAIA ICICGGIAGI GGGATACGAC GATACCGAAG ACAGCTCATG TTATATCCCG CCGTTAACCA CCATCAAACA GGATTITICGC CIGCIGGGGC AAACCAGCGI GGACCGCTIG CIGCAACTCI CICAGGGCCA GTATGCCGGT GTCTTTATC AGACCGTTTC CCGCGTGGTG AACCAGGCCA AATGCTGAAT GAGGGCATCG TTCCCACTGC GATGCTGGTT 2161 2341 2401 2461 2521 2581 2641 2701 3121 3241 2881 3001 3061 3181

GGCGGTGAAG GGCAATCAGC TGTTGCCCGT CTCACTGGTG AAAAGAAAAA CCACCCTGGC GCCCAATACG CAAACCGCCT CTCCCGCGC GTTGGCCGAT TCATTAATGC AGCTGGCACG ACAGGITICC CGACIGGAAA GCGGGCAGIG AGCGCAACGC AATTAAIGIG AGITAGCICA CTCATTAGGC ACCCCAGGCT TTACACTTTA TGCTTCCGGC TCGTATGTTG TGTGGAATTG TTCACTGGCC CAACAGTIGC GCAGCCIGAA IGGCGAAIGG CGCITIGCCI GGIITICCGGC ACCAGAAGCG GTCGTITTAC AACGICGIGA CTGGGAAAAC CCTGGCGTTA CCCAACTTAA TCGCCTTGCA GCACATCCCC CITICGCCAG CIGGCGTAAT AGCGAAGAGG CCCGCACCGA ICGCCCTICC GTGCCGGAAA GCTGGCTGGA GTGCGATCTT CCTGAGGCCG ATACTGTCGT CGTCCCCTCA AACTGGCAGA TGCACGGTTA CGATGCGCCC ATCTACACCA ACGTAACCTA TCCCATTACG GTCAATCCGC CGTTTGTTCC CACGGAGAAT CCGACGGGTT GTTACTCGCT CACATTTAAT AGCTTATCGA CTGCACGGTG CACCAATGCT TCTGGCGTCA GGCAGCCATC GGAAGCTGTG TTGTATGAGC GTTGATGAAA GCTGGCTACA GGAAGGCCAG ACGCGAATTA TTTTTGATGG CGTTGGAATT TCTGGATAAT GITTTTTGCG CCGACATCAT AACGGTTCTG GCAAATATTC TGAAATGAGC TGTTGACAAT TAATCATCGG CTCGTATAAT GTGTGGAATT GTGAGCGGAT AACAATTTCA CACAGGAAAC AGTATTCATG TCCCCTATAC TAGGTTATTG GAAAATTAAG GGCCTTGTGC GCGATGAAGG TGATAAATGG CGAAACAAAA AGTTTGAATT GGGTTTGGAG TTTCCCAATC GTATGGCTGT GCAGGTCGTA AATCACTGCA TAATTCGTGT CGCTCAAGGC GCACTCCCGT TGAGCGGATA ACAATTTCAC ACAGGAAACA GCTATGACCA TGATTACGGA AACCCACTCG ACTTCTTTG GAATATCTTG AAGAAAAAA TGAAGAGCAT 3301 3361 3421 3481 3541 3601 3661 3721 3841 3901 4021 4141 4201 3961 4081 4261 4321 4381

	CAGG	GTGGGATCCC	ATCGAAGGTC	ATCCTCCAAA ATCGGATCTG ATCGAAGGTC GTGGGATCCC CAGG	ATCCTCCAAA	4921
GGTGGCGACC	CACGTTTGGT	GCTGGCAAGC	CCTTTGCAGG	CCAGCAAGTA TATAGCATGG CCTTTGCAGG GCTGGCAAGC CACGTTTGGT GGTGGCGACC	CCAGCAAGTA	4861
TACTTGAAAT	AATTGATAAG	TITIAAAAAA CGTATIGAAG CTAICCCACA AATIGAIAAG IACTIGAAAI	CGTATTGAAG	TTTAAAAAA	AATTAGTTTG	4801
GCGTTCCCAA	GIGCCIGGAI	TGGACCCAAT	GTTTTATACA	TGTATGACGC TCTTGATGTT GTTTTATACA TGGACCCAAT GTGCCTGGAT GCGTTCCCAA	TGTATGACGC	4741
GACTTCATGT	AACCCATCCT	GTGATCATGT	TATTTAAATG	ATCGTTTATG TCATAAAACA TATTTAAATG GTGATCATGT AACCCATCCT GACTTCATGT	ATCGTTTATG	4681
TTGAAACTCT CAAAGTTGAT TTTCTTAGCA AGCTACCTGA AATGCTGAAA ATGTTCGAAG	AATGCTGAAA	AGCTACCTGA	TTTCTTAGCA	CAAAGTTGAT	TTGAAACTCT	4621
AGTAAAGACT	AATTGCATAT	GTGTTTCGAG	ATTAGATACG	TTGAAGGAGC GGTTTTGGAT ATTAGATACG GTGTTTCGAG AATTGCATAT AGTAAAGACT	TTGAAGGAGC	4561
TAGCTGACAA GCACAACATG TTGGGTGGTT GTCCAAAAGA GCGTGCAGAG ATTTCAATGC	GCGTGCAGAG	GTCCAAAAGA	TTGGGTGGTT	GCACAACATG	TAGCTGACAA	4501
TTCCTTATTA TATTGATGGT GATGTTAAAT TAACACAGTC TATGGCCATC ATACGTTATA	TATGGCCATC	TAACACAGTC	GATGTTAAAT	TATTGATGGT	TTCCTTATTA	4441

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<del>, -1</del>	AGCTTATCGA	CTGCACGGTG	CACCAATGCT	AGCTTATCGA CTGCACGGTG CACCAATGCT TCTGGCGTCA GGCAGCCATC GGAAGCTGTG	GGCAGCCATC	GGAAGCTGTG
61	GTATGGCTGT	GCAGGTCGTA	AATCACTGCA	GTATGGCTGT GCAGGTCGTA AATCACTGCA TAATTCGTGT CGCTCAAGGC	CGCTCAAGGC	GCACTCCCGT
121	TCTGGATAAT	GTTTTTGCG	CCGACATCAT	AACGGTTCTG	GCAAATATTC	TGAAATGAGC
. 181	TGTTGACAAT	TAATCATCGG	CTCGTATAAT	GTGTGGAATT	GTGAGCGGAT AACAATTTCA	AACAATTTCA
241	CACAGGAAAC	AGTATTCATG	TCCCCTATAC	TAGGTTATTG	GAAAATTAAG	GGCCTTGTGC
301	AACCCACTCG	ACTICTITIG	GAATATCTTG	ААСАААААТА	TGAAGAGCAT	TTGTATGAGC
361	GCGATGAAGG	TGATAAATGG	CGAAACAAAA	AGTTTGAATT	GGGTTTGGAG	TTTCCCAATC
421	TTCCTTATTA	TATTGATGGT	GATGTTAAAT	TAACACAGTC	TATGGCCATC	ATACGTTATA
481	TAGCTGACAA	GCACAACATG	TTGGGTGGTT	GTCCAAAAGA GCGTGCAGAG	GCGTGCAGAG	ATTTCAATGC
541	TTGAAGGAGC	GGTTTTGGAT	ATTAGATACG	TTGAAGGAGC GGTTTTGGAT ATTAGATACG GTGTTTCGAG AATTGCATAT		AGTAAAGACT
601	TTGAAACTCT	CAAAGTTGAT	TTTCTTAGCA	TIGAAACICI CAAAGIIGAI TITCITAGCA AGCIACCIGA AAIGCIGAAA		ATGTTCGAAG
661	ATCGTTTATG	TCATAAAACA	TATTTAAATG	GTGATCATGT	AACCCATCCT	GACTTCATGT
721	TGTATGACGC	TCTTGATGTT	GTTTTATACA	TGGACCCAAT	GTGCCTGGAT	GCGTTCCCAA
781	AATTAGTTTG	TTTAAAAAA	CGTATTGAAG	CTATCCCACA	AATTGATAAG	TACTTGAAAT
841	CCAGCAAGTA	TATAGCATGG	CCTTTGCAGG	GCTGGCAAGC	CACGITIGGI (	GGTGGCGACC
901	ATCCTCCAAA	ATCGGATCTG	ATCGAAGGTC	GTGGGATCCC	CAGGAATTCC	ATGAGTGAGG
961	CCCGCAGGGA	CAGCACGAGC	AGCCTGCAGC	GCAAGAAGCC ACCCTGGCTA	ACCCTGGCTA 7	AAGCTGGACA
1021	Treceretee	ветессств	ACGCCAGAAG	TTCCCTCTGC GGTGCCCCTG ACGCCAGAAG AGCCCAGCTT CCTGCAGCCC		CTGAGGCGAC

CCTTCTTCAC CTACTGGCTT ACCTTCGTGC ACTCGCTCGT CACCATCCTA GCCGTGTGCA	2161 CC
ACCGCAAGCG CATCGACAGC TTCGTCAAGC GCCAGATCGA GGACATGGAC GACCACAGGC	2101 AC
TCGCCCGGGA GAAGCGGCCG TATGGGCTGG GCATGGTGGG ACGGCTCACC AACCGCACCT	2041 T
TEGIGAGCAC CECEGEGECE CGACGEGEC AGCGIAICEC GGIGCCGGIG CGCAAGCICI	1981 TC
GGCGGAAGCA GAAGGAGGGC GCCGCAGCCC CGCAGCCCAA GGTGCGGCTC CGACAGGAGG	1921 G
GGGCCCTGGA CCGCAGCGAG CTTGAGCGCA GCCACCTGAT GCTGCCCTTG GAGCGAGGCT	1861 G
CATCGGAGGC AGCGCTAAAG GACTGGGAGA AGGCACCGGA GCAGGCGGAC CTCACCGGCG	1801 C
CCCGGGAAGG TATCCTCCAT GAAGAGCTGT CCACATACCC GGATGAAGTT TTCGAGTCCC	1741 C
CTAGCTTTCT GGAGGAGGAC ACAACTGATT TCCCCGATGA GCTGGACACA TCCTTCTTTG	1681 C
AAGGCCGCTC CGTTAGGGAT GGCACCTTTC GCCGGGCACG GCGTCGAAGC TTCACTCCAG	1621 A
GGCGGCGCAA GCGAGAGTCG GTGGCCAAGA TGAGCTTCCG GGCGGCCGCA GCGCTGATGA	1561 G
CGGGTGCTGC CTCCCTCTGC TCCTTCTCCA GCTCCCGCTC AGGTTTCCAC CGGCTCCCGC	1501 C
CCTTCCGTGT GGCAGATGAC ACTGCGGAAG GCCTGAGTGC CCCACACACT CCCGTCACGC	1441 C
ACGIGGGGCC AIGCCAGCIG GGCAIGCAGA AGAICAIAGA CCCCCIGGCC CGIGGCCGIG	1381 A
TGGACCTGCC CAGCCAGGAC AACGTGTCGC TGACCAGCAC CGAGACGCCA CCCCCACTCT	1321 T
AGAGCATCCG TCACTGCAGC CAGCGCTACG GGAAGCTGAA GCCCCAGGTC CTCCGGGAGC	1261 A
GGACCGCCGA CTGGTTTGGA GTGAGCAAGG ACAGTGACAG CACCCAGAAA TGGCAGCGCA	1201 G
ATGAGCTCCG GCGGCCGGTG CTGCAACGCC AGACGTCCAT CACACAGACC ATCCGCAGGG	1141 A
AGGCTTTCCT GAGGAGTGTG AGTATGCCAG CCGAGACAGC CCACATCTCT TCACCCCACC	1081 A

TCTATGGCAT CGCGCCCGTG GGCTTCTCGC AGCATGAGAC GGTGGACTCG GTGCTGCGGA GCAACGACAG GTCGGGCTGC GTGCAGACCT CGGAGGAGGA GTGCTCGTCC ACGCTGGCAG ACCGCGGGGT CTACGAGAAC GTCAAGTACG TGCAGCAGGA GAACTTCTGG ATCGGGCCCA CIGCAIGCGC CAGGACCCGC AGGIGCACAG CITCAITCGC ICGGCGCGCG AGCGCGAGAA GCACICCGCC IGCIGCGIGC TGTGGGTGAA GTGGCCCATC CATCCCAGCG CCCCAGAGCT TGCGGGCCAC AAGAGACAGT TIGGCICIGI CIGCCACCAG GAICCCAGGI GAGICGACIC GAGCGGCCGC AICGIGACIG ACTGACGATC TGCCTCGCGC GTTTCGGTGA TGACGGTGAA AACCTCTGAC ACATGCAGCT CCCGGAGACG GTCACAGCTT GTCTGTAAGC GGATGCCGGG AGCAGACAAG CCCGTCAGGG CGCGTCAGCG GGTGTTGGCG GGTGTCGGGG CGCAGCCATG ACCCAGTCAC GTAGCGATAG CGGAGTGTAT AATTCTTGAA GACGAAAGGG CCTCGTGATA CGCCTATTTT TATAGGTTAA CTIAGACGIC AGGIGGCACT TITCGGGGAA AIGIGCGCGG AACCCCTATT IGTTTATTTT ICTAAATACA ITCAAATATG TATCCGCTCA IGAGACAATA ACCCTGATAA ATGCTTCAAT AATATTGAAA AAGGAAGAGT ATGAGTATTC AACATTTCCG GTTTTTGCTC ACCCAGAAAC GGATCTCAAC AGCGGTAAGA TCCTTGAGAG TTTTCGCCCC GAAGAACGTT TTCCAATGAT CACCAGTCAC GCTGGTGAAA GTAAAAGATG CTGAAGATCA GTTGGGTGCA CGAGTGGGTT ACATCGAACT CGTGTTGACG CCGGGCAAGA GCAACTCGGT CGCCGCATAC ACTATTCTCA GAATGACTTG GTTGAGTACT GCTCGGAGGC CCTCATCCAC CTGGGCGCCA AGTTTTCGCC GAGCACTITI AAAGIICIGC IAIGIGGCGC GGIAITAICC TGTCGCCCTT ATTCCCTTTT TTGCGGCATT TTGCCTTCCT TGTCATGATA ATAATGGTTT 2221 2341 2641 2401 2461 2521 2581 2761 2701 2821 2881 3241 3301 3061 3121 3181

GAGTGATAAC ACTGCGGCCA ACTTACTTCT GACAACGATC GGAGGACCGA AGGAGCTAAC AGAAAAGCAT CTTACGGATG GCATGACAGT AAGAGAATTA TGCAGTGCTG CCATAACCAT GAATGAAGCC ATACCAAACG ACGAGCGTGA CACCACGATG CCTGCAGCAA TGGCAACAAC CGCTTTTTTG CACAACATGG GGGATCATGT AACTCGCCTT GATCGTTGGG AACCGGAGCT GTTGCGCAAA CTATTAACTG GCGAACTACT TACTCTAGCT TCCCGGCAAC AATTAATAGA GGGCCCAGAT GGTAAGCCCT CCCGTATCGT AGTTATCTAC ACGACGGGA GTCAGGCAAC CIGGAIGGAG GCGGAIAAAG IIGCAGGACC ACTICIGCGC ICGGCCCTIC CGGCIGGCIG TIGCAGCACT TATGGATGAA CGAAATAGAC AGATCGCTGA GATAGGTGCC TCACTGATTA AGCATTGGTA ACTGICAGAC CAAGITIACI CAIATAIACI TIAGAIIGAI ITAAAACIIC AITIIIAAII TAAAAGGATC TAGGTGAAGA TCCTTTTTGA TAATCTCATG ACCAAAATCC CTTAACGTGA CACTGAGCGT CAGACCCCGT AGAAAGATC AAAGGATCTT CTTGAGATCC TITITITICIG CGCGIAAICI GCIGCIIGCA AACAAAAAA CCACCGCIAC CAGCGGIGGI TITICCGAAG GTAACTGGCT TCAGCAGAGC TCAAGAACTC TGTAGCACCG CCTACATACC TCGCTCTGCT AATCCTGTTA CCAGTGGCTG CTGCCAGTGG CGATAAGTCG TGTCTTACCG GGTTGGACTC AAGACGATAG TTACCGGATA AGGCGCAGCG ACTGAGATAC CTACAGCGTG AGCTATGAGA AAGCGCCACG CTTCCCGAAG GGAGAAAGGC GTCGGGCTGA ACGGGGGTT CGTGCACACA GCCCAGCTTG GAGCGAACGA CCTACACCGA CGCGGTATCA GCAGATACCA AATACTGTCC TTCTAGTGTA GCCGTAGTTA GGCCACCACT GTTTATTGCT GATAAICTG GAGCCGGTGA GCGTGGGTCT TIGITIGCCG GAICAAGAGC IACCAACICI GTTTTCGTTC 3361 3781 3841 3421 3541 3601 3661 3901 3721 3961 4081 4141 4021 4201 4261 4321 4381

1

GGACAGGTAT CCGGTAAGCG GCAGGGTCGG AACAGGAGAG CGCACGAGGG AGCTTCCAGG GGGAAACGCC TGGTATCTTT ATAGTCCTGT CGGGTTTCGC CACCTCTGAC TTGAGCGTCG TGATICIGIG GAIAACCGIA TIACCGCCII IGAGIGAGCI GAIACCGCIC GCCGCAGCCG TITACGGITC CIGGCCITIT GCIGGCCITT IGCICACAIG ITCTITCCIG CGITAICCCC ATTITIGIGA IGCICGICAG GGGGGGGAG CCIATGGAAA AACGCCAGCA ACGCGGCCIT TICCCGCGTG GTGAACCAGG CCAGCCACGI TTCTGCGAAA ACGCGGGAAA AAGTGGAAGC AACGACCGAG CGCAGCGAGT CAGTGAGCGA GGAAGCGGAA GAGCGCCTGA TGCGGTATTT TCGAATGGTG CAAAACCITT CGCGGTAIGG CAIGAIAGCG CCCGGAAGAG AGICAAIICA GGGIGGIGAA TGTGAAACCA GTAACGTTAT ACGATGTCGC AGAGTATGCC GGTGTCTCTT ATCAGACCGT GGCGATGGCG GAGCTGAATT ACATTCCCAA CCGCGTGGCA CAACAACTGG CGGGCAAACA ACGAAGCGGC GTCGAAGCCT GTAAAGCGGC GGTGCACAAT CTTCTCGCGC AACGCGTCAG GTCGTIGCIG ATTGGCGTIG CCACCTCCAG ICTGGCCCCTG CACGCGCCGT CGCAAAITGI CGCGGCGATT AAATCTCGCG CCGATCAACT GGGTGCCAGC GTGGTGGTGT CGATGGTAGA TGGGCTGATC ATTAACTATC CGCTGGATGA CCAGGATGCC ATTGCTGTGG AAGCTGCCTG CACTAATGIT CCGGCGTTAT TICTTGATGI CTCTGACCAG ACACCCATCA ACAGTAITAI TITCICCCAI GAAGACGGIA CGCGACIGGG CGIGGAGCAI CIGGICGCAI IGGGICACCA GCAAATCGCG CIGITAGCGG GCCCAITAAG ITCIGICICG GCGCGICIGC GICIGGCIGG CTGGCATAAA TATCTCACTC GCAATCAAAT TCAGCCGATA GCGGAACGGG AAGGCGACTG TCTCCTTACG CATCTGTGCG GTATTTCACA CCGCATAAAT TCCGACACCA 4501 4561 4621 4681 4741 4801 4861 4921 4981 5041 5101 5161 5221 5341 5401 5281

	TTATTTTGA TGGCGTTGGA ATT	CAGACGCGAA 1	6601
AATGTTGATG AAAGCTGGCT ACAGGAAGGC	GTTGTTACTC GCTCACATTT AA1	AATCCGACGG G	6541
ACGGTCAATC CGCCGTTTGT TCCCACGGAG	CCAACGIAAC CTAICCCAIT ACC	CCCATCTACA C	6481
TCAAACTGGC AGATGCACGG TTACGATGCG	CCGATACTGT CGTCGTCCC TC2	CITCCIGAGG (	6421
GCGGTGCCGG AAAGCTGGCT GGAGTGCGAT	CCTGGTTTCC GGCACCAGAA GCC	rececritie (	6361
TCCCAACAGT TGCGCAGCCT GAATGGCGAA	AATAGCGAAG AGGCCCGCAC CGATCGCCCT TC	AATAGCGAAG A	6301
GCAGCACATC CCCCTTTCGC CAGCTGGCGT	TTACCCAACT TAATCGCCTT GC	AACCCTGGCG 1	6241
GCCGTCGTTT TACAACGTCG TGACTGGGAA	CCATGATTAC GGATTCACTG GC	ACAGCTATGA (	6181
TTGTGAGCGG ATAACAATTT CACACAGGAA	TTGTGTGGAA	TTATGCTTCC GGCTCGTATG	6121
CTCATTA GGCACCCCAG GCTTTACACT	GTGAGCGCAA CGCAATTAAT GTGAGTTAGC TCACTCATTA GGCACCCCAG	GTGAGCGCAA (	6061
ACGACAGGIT TCCCGACTGG AAAGCGGGCA	GATTCATTAA TGCAGCTGGC AC	CGCGTTGGCC	6001
GGCGCCCAAT ACGCAAACCG CCTCTCCCCG	GTGAAAAGAA AAACCACCCT GG	CGTCTCACTG (	5941
CCAGGCGGTG AAGGGCAATC AGCTGTTGCC	TIGCIGCAAC ICICICAGGG CC	CGTGGACCGC	5881
GGATTTT CGCCTGC GGCAAACCAG	ATGTTATATC CCGCCGTTAA CCACCATCAA ACAGGATTTT	ATGTTATATC (	5821
ATATCTCGGT AGTGGGATAC GACGATACCG AAGACAGCTC	GTTGGTGCGG ATATCTCGGT AG	CGGGCTGCGC	5761
GCTGGGCGCA ATGCGCGCCA TTACCGAGTC	GTTGCCAACG ATCAGATGGC GC	TGCGATGCTG (	5701
GAGTGCCATG ICCGGTTTTC AACAACCAT GCAAATGCTG AATGAGGGCA ICGTTCCCAC	TCCGGTTTTC AACAAACCAT GC	GAGTGCCATG	5641

FIG. 29, (SEQ ID NO:64) Coding region for the C terminus 375 aa: 945-2069

Н	AGCTTATCGA	CTGCACGGTG	CACCAATGCT	TCTGGCGTCA	AGCITATCGA CIGCACGGIG CACCAAIGCT ICIGGCGICA GGCAGCCAIC GGAAGCIGIG	GGAAGCTGTG
61	GTATGGCTGT	GCAGGTCGTA	GCAGGICGIA AAICACIGCA	TAATTCGTGT	TAATTCGTGT CGCTCAAGGC GCACTCCCGT	GCACTCCCGT
121	TCTGGATAAT	GTTTTTGCG	CCGACATCAT	AACGGTTCTG	GCAAATATTC	TGAAATGAGC
181	TGTTGACAAT	TAATCATCGG	CTCGTATAAT	GTGTGGAATT	GTGAGCGGAT	AACAATTTCA
241	CACAGGAAAC	AGTATTCATG	TCCCCTATAC	TAGGTTATTG	GAAAATTAAG	GGCCTTGTGC
301	AACCCACTCG	ACTTCTTTG	GAATATCTTG	AAGAAAATA	TGAAGAGCAT	TTGTATGAGC
361	GCGATGAAGG	GCGATGAAGG TGATAAATGG	CGAAACAAAA	AGTTTGAATT	GGGTTTGGAG	TTTCCCAATÇ
421	TTCCTTATTA	TATTGATGGT	GATGTTAAAT	TAACACAGTC	TATGGCCATC	ATACGTTATA
481	TAGCTGACAA	TAGCTGACAA GCACAACAIG	TTGGGTGGTT		GTCCAAAAGA GCGTGCAGAG	ATTTCAATGC
541	TTGAAGGAGC		ATTAGATACG	GTGTTTCGAG	GGTTTTGGAT ATTAGATACG GTGTTTCGAG AATTGCATAT AGTAAAGACT	AGTAAAGACT
601	TTGAAACTCT	TTGAAACTCT CAAAGTTGAT	TTTCTTAGCA	AGCTACCTGA	TTTCTTAGCA AGCTACCTGA AATGCTGAAA ATGTTCGAAG	ATGTTCGAAG
199	ATCGTTTATG	TCATAAAACA	TATTTAAATG	GTGATCATGT	TCATAAAACA TATTTAAATG GTGATCATGT AACCCATCCT GACTTCATGT	GACTTCATGT
721	TGTATGACGC	TGTATGACGC TCTTGATGTT GTTTTATACA TGGACCCAAT	GTTTTATACA		GTGCCTGGAT (	GCGTTCCCAA
781	AATTAGTTTG		TTTTAAAAA CGTATTGAAG	CTATCCCACA AATTGATAAG		TACTTGAAAT
841	CCAGCAAGTA	TATAGCATGG	CCTTTGCAGG	CCTTTGCAGG GCTGGCAAGC CACGTTTGGT		GGTGGCGACC
901	ATCCTCCAAA	ATCCTCCAAA ATCGGATCTG ATCGAAGGTC		GTGGGATCCC	CAGGAATTCC (	CAGGTGCACA
961	GCTTCATTCG	CTCGGCGCGC GAGCGCGAGA AGCACTCCGC	GAGCGCGAGA	AGCACTCCGC	CTGCTGCGTG (	CGCAACGACA
1021	GGTCGGGCTG	CGTGCAGACC	TCGGAGGAGG	AGTGCTCGTC	GGTCGGGCTG CGTGCAGACC TCGGAGGAGG AGTGCTCGTC CACGCTGGCA GTGTGGGTGA	STGTGGGTGA

AGIGGCCCAI CCAICCCAGC GCCCCAGAGC TIGCGGGCCA CAAGAGACAG ITIGGCICIG CAGAAGACAT CACCAAGIGG CCGAICIGCA CCAAAAACAG CGCIGGGAAC CACACCAACC GAGGAGGCCA TCTGCCACCA GGATCCCAGG GTGTGTGATG AGCCCTCCTC CGAAGACCCT CATGAGTGGC ATCCCCACAT GGACTGTGTC ATCACAGGAC GGCCCTGCTG CATTGGCACC AAGGGCAGGT CGCTCTGCTC TCAGGTGCAC TGCATGGATG ATGTGTGGG GCTCCTGCCT TTTCTCAACC CCGAGGIGCC IGACCAGITC TACCGCCIGI GGCIAICCCI CIICCIGCAC GCCGGGAICI TGCACTGCCT GGTGTCCATC TGCTTCCAGA TGACTGTCCT GCGGGACCTG GAGAAGCTGG CAGGCTGGCA CCGCATAGCC ATCATCTACC TGCTGAGTGG TGTCACCGGC AACCTGGCCA GTGCCATCTT CCTGCCATAC CGAGCAGAGG TGGGTCCTGC TGGCTCCCAG TTCGGCATCC TGGCCTGCCT CTTCGTGGAG CTCTTCCAGA GCTGGCAGAT CCTGGCGCGG CCCTGGCGTG CCTICITCAA GCIGCIGGCI GIGGIGCICI ICCICIICAC CITIGGGCIG CIGCCGIGGA TIGACAACIT IGCCCACAIC ICGGGGIICA ICAGIGGCCI CIICCICICC IICGCCIICI TGCCCTACAT CAGCTTTGGC AAGTTCGACC TGTACCGGAA ACGCTGCCAG ATCATCATCT TICAGGIGGI CIICCIGGGC CICCIGGCIG GCCIGGIGGI CCICIICIAC GICIAICCIG TCGGCTGTGA GTGGTGTGAG TTCCTCACCT GCATCCCCTT CACTGACAAG TTCTGTGAGA AGTACGAACT GGACGCTCAG CTCCACTGAG TCGACTCGAG CGGCCGCATC GTGACTGACT GACGATCTGC CTCGCGCGTT TCGGTGATGA CGGTGAAAAC CTCTGACACA TGCAGCTCCC GGAGACGGTC ACAGCTIGIC IGIAAGCGGA IGCCGGGAGC AGACAAGCCC GICAGGGCGC GTGAGATCAC CTCCCGGGAG TACTGTGACT TCATGAGGGG CTACTTCCAT 1081 1201 1261 1321 1381 1441 1501 1561 1621 1681 1741 1801 1861 1921 2041 2101 2161

GTCAGCGGGT GITGGCGGGT GICGGGCGC AGCCATGACC CAGTCACGIA GCGATAGCGG CATGATAATA ATGGTTTCTT AGACGTCAGG TGGCACTTTT CGGGGAAATG TGCGCGGAAC CCCTATITICI ITAITITICI AAATACAITC AAAIAIGIAI CCGCICAIGA GACAAIAACC TCTCAACAGC GGTAAGATCC TTGAGAGTTT TCGCCCCGAA GAACGTTTTC CAATGATGAG AGTGTATAAT ICTTGAAGAC GAAAGGGCCT CGTGATACGC CTATTTTAT AGGTTAATGT CTGATAAATG CTTCAATAAT ATTGAAAAG GAAGAGTATG AGTATTCAAC ATTTCCGTGT TCGAACTGGA CACTITIAAA GITCIGCIAI GIGGCGCGGI ATTAICCCGI GITGACGCCG GGCAAGAGCA ACTCGGTCGC CGCATACACT ATTCTCAGAA TGACTTGGTT GAGTACTCAC CAGTCACAGA AAAGCATCTT ACGGATGGCA TGACAGTAAG AGAATTATGC AGTGCTGCCA TAACCATGAG CGCCCTTATT CCCTTTTTG CGGCATTTTG CCTTCCTGTT TTTGCTCACC CAGAAACGCT TGATAACACT GCGGCCAACT TACTTCTGAC AACGATCGGA GGACCGAAGG AGCTAACCGC TITITIGCAC AACAIGGGGG AICAIGIAAC ICGCCIIGAI CGIIGGGAAC CGGAGCIGAA TGAAGCCATA CCAAACGACG AGCGTGACAC CACGATGCCT GCAGCAATGG CAACAACGTT GCGCAAACTA TTAACTGGCG AACTACTTAC TCTAGCTTCC CGGCAACAAT TAATAGACTG GCCAGAIGGI AAGCCCICCC GIAICGIAGI IAICIACACG ACGGGGAGIC AGGCAACIAI CTGGCTGGTT TATIGCIGAT AAAICIGGAG CCGGIGAGCG IGGGICICGC GGIAICAIIG CAGCACIGGG GGATGAACGA AATAGACAGA TCGCTGAGAT AGGTGCCTCA CTGATTAAGC ATTGGTAACT GGTGAAAGTA AAAGATGCTG AAGATCAGTT GGGTGCACGA GTGGGTTACA GATGGAGGCG GATAAAGTTG CAGGACCACT TCTGCGCTCG GCCCTTCCGG 2221 2521 2341 2401 2461 2581 2641 2701 2821 2941 3061 3001 3121 3181 3241 3301

GAAACCAGTA ACGITATACG ATGICGCAGA GTAIGCCGGI GICTCTTAIC AGACCGITIC	4441 G
AACCITICGC GGIAIGGCAI GAIAGCGCCC GGAAGAGAGI CAATICAGGG IGGIGAAIGI	4381 A
CCTTACGCAT CTGTGCGGTA TTTCACACCG CATAAATTCC GACACCATCG AATGGTGCAA	4321 C
GACCGAGCGC AGCGAGTCAG TGAGCGAGGA AGCGGAAGAG CGCCTGATGC GGTATTTTCT	4261 G
ITCIGIGGAI AACCGIAITA CCGCCITIGA GIGAGCIGAI ACCGCICGCC GCAGCCGAAC	4201 I
ACGGTTCCTG GCCTTTTGCT GGCCTTTTGC TCACATGTTC TTTCCTGCGT TATCCCCTGA	4141 P
TTTGTGATGC TCGTCAGGGG GGCGGAGCCT ATGGAAAAAC GCCAGCAACG CGGCCTTTTT	4081 1
AAACGCCTGG TATCTTTATA GTCCTGTCGG GTTTCGCCAC CTCTGACTTG AGCGTCGALT	4021
CAGGTATCCG GTAAGCGGCA GGGTCGGAAC AGGAGACGC ACGAGGGAGC TTCCAGGGGG	3961 (
GAGATACCTA CAGCGTGAGC TATGAGAAAG CGCCACGCTT CCCGAAGGGA GAAAGGCGGA	3901 (
GGGCTGAACG GGGGGTTCGT GCACACACC CAGCTTGGAG CGAACGACCT ACACCGAACT	3841 (
TAAGICGIGI CITACCGGGI IGGACICAAG ACGAIAGITA CCGGAIAAGG CGCAGCGGIC	3781
AGCACCGCCT ACATACCTCG CTCTGCTAAT CCTGTTACCA GTGGCTGCTG CCAGTGGCGA	3721
GATACCAAAT ACTGTCCTTC TAGTGTAGCC GTAGTTÄGGC CACCACTTCA AGAACTCTGT	3661 (
TITGCCGGAT CAAGAGCTAC CAACTCTITT TCCGAAGGTA ACTGGCTTCA GCAGAGCGCA	3601
TITICIGCGC GTAAICTGCT GCTIGCAAAC AAAAAAACCA CCGCTACCAG CGGTGGITIG	3541
TICGIICCAC IGAGCGICAG ACCCCGIAGA AAAGAICAAA GGAICIICII GAGAICCIII	3481
AAGGATCTAG GTGAAGATCC TTTTTGATAA TCTCATGACC AAAATCCCTT AACGTGAGTT	3421
GICAGACCAA GITTACICAT ATATACITTA GAITGAITTA AAACITCAIT ITTAAITTAA	3361

CCGCGTGGTG AACCAGGCCA GCCACGTTTC TGCGAAAACG CGGGAAAAAG TGGAAGCGGC GCAAACAGTC GTIGCTGAIT GGCGTIGCCA CCICCAGICI GGCCCTGCAC GCGCCGICGC AAAIIGICGC TGGTAGAACG AAGCGGCGTC GAAGCCTGTA AAGCGGCGGT GCACAATCTT CTCGCGCAAC GCGTCAGTGG GCTGATCATT AACTATCCGC TGGATGACCA GGATGCCATT GCTGTGGAAG CTGCCTGCAC TAAIGIICCG GCGTIAITIC ITGAIGICIC IGACCAGACA CCCAICAACA GIAITAITII CTCCCATGAA GACGGTACGC GACTGGGCGT GGAGCATCTG GTCGCALTGG GTCACCAGCA AATCGCGCTG TTAGCGGGCC CATTAAGTTC TGTCTCGGCG CGTCTGCGTC TGGCTGGCTG GCATAAATAT CTCACTCGCA ATCAAATTCA GCCGATAGCG GAACGGGAAG GCGACTGGAG TGCCATGTCC GGTTTTCAAC AAACCATGCA AATGCTGAAT GAGGGCATCG TTCCCACTGC GATECTGGTT GCCAACGATC AGATGGCGCT GGGCGCAATG CGCGCCATTA CCGAGTCCGG GCTGCGCGTT GGTGCGGATA TCTCGGTAGT GGGATACGAC GATACCGAAG ACAGCTCATG CICCCCGCGC TTATATCCCG CCGTTAACCA CCATCAAACA GGATTTTCGC CTGCTGGGGC AAACCAGCGT GGACCGCTTG CTGCAACTCT CTCAGGGCCA GGCGGTGAAG GGCAATCAGC TGTTGCCCGT GTIGGCCGAI ICAITAAIGC AGCIGGCACG ACAGGIIICC CGACIGGAAA GCGGGCAGIG TGCTTCCGGC TCGTATGTTG TGTGGAATTG TGAGCGGATA ACAATTTCAC ACAGGAAACA TTACACTTTA GATGGCGGAG CTGAATTACA TTCCCAACCG CGTGGCCACAA CAACTGGCGG GGCGATTAAA TCTCGCGCCG ATCAACTGGG TGCCAGCGTG GTGGTGTCGA CTCACTGGTG AAAAGAAAAA CCACCCTGGC GCCCAATACG CAAACCGCCT AGCGCAACGC AATTAATGTG AGTTAGCTCA CTCATTAGGC ACCCCAGGCT 4501 4561 4621 4741 4801 4861 4921 4981 5041 5101 5341 5161 5221 5281 5401

			CGTTGGAATT	ACGCGAATTA TTTTGATGG CGTTGGAATT	ACGCGAATTA	6061
GGAAGGCCAG	GCTGGCTACA	GTTGATGAAA	CACATTTAAT	CCGACGGGTT GTTACTCGCT CACATTTAAT GTTGATGAAA GCTGGCTACA GGAAGGCCAG	CCGACGGGTT	6001
CACGGAGAAT	CGTTTGTTCC	GTCAATCCGC	TCCCATTACG	ATCTACACCA ACGTAACCTA TCCCATTACG GTCAATCCGC CGTTTGTTCC CACGGAGAAT	ATCTACACCA	5941
CGATGCGCCC	TGCACGGTTA	AACTGGCAGA	CGTCCCCTCA	CCTGAGGCCG ATACTGTCGT CGTCCCCTCA AACTGGCAGA TGCACGGTTA CGATGCGCCC	CCTGAGGCCG	5881
GTGCGATCTT	GCTGGCTGGA	GTGCCGGAAA	ACCAGAAGCG	CGCTTTGCCT GGTTTCCGGC ACCAGAAGCG GTGCCGGAAA GCTGGCTGGA GTGCGATCTT	CGCTTTGCCT	5821
TGGCGAATGG	GCAGCCTGAA	CAACAGITGC	TCGCCCTTCC	AGCGAAGAGG CCCGCACCGA TCGCCCTTCC CAACAGTTGC GCAGCCTGAA TGGCGAATGG	AGCGAAGAGG	5761
CTGGCGTAAT	CTTTCGCCAG	GCACATCCCC	TCGCCTTGCA	CCTGGCGTTA CCCAACTTAA TCGCCTTGCA GCACATCCCC CTTTCGCCAG CTGGCGTAAT	CCTGGCGTTA	5701
CTGGGAAAAC	AACGTCGTGA	GTCGTTTTAC	TTCACTGGCC	GCTATGACCA TGATTACGGA TTCACTGGCC GTCGTTTTAC AACGTCGTGA CTGGGAAAAC		5641

FIG. 30, (SEQ ID NO:66) ICT1024 coding region: 310-2879

Н	TAATACGACT	CACTATAGGG	GAATTGTGAG	TAATACGACT CACTATAGGG GAATTGTGAG CGGATAACAA	TTCCCCTCTA GACTTACAAT	GACTTACAAT
61	TTCCATTCGC	CATTCAGGCT	GCGCAACTGT	GCGCAACTGT TGGGAAGGGC	GAICGGIACG GGCCICITCG	GGCCTCTTCG
121	CTATTACGCC	AGCTTGCGAA	сестесетес	CTATTACGCC AGCTTGCGAA CGGTGGGTGC GCTGCAAGGC GATTAAGTTG GGTAACGCCA	GATTAAGTTG	GGTAACGCCA
181	GGATTCTCC	AGTCACGACG	TTGTAAAACG	GGATTCTCCC AGTCACGACG TTGTAAAACG ACGGCCAGCG AGAGATCTTG ATTGGCTAGC	AGAGATCTTG	ATTGGCTAGC
241	AGAATAATTT	TGTTTAACTT	TAAGAAGGAG	TGTTTAACTT TAAGAAGAG ATATACCATG GCGATATCCC GGGAGCTCGT	GCGATATCCC	GGGAGCTCGT
301	GGATCCGAAT	TCCATGAGTG	AGGCCCGCAG	GGACAGCACG AGCAGCCTGC AGCGCAAGAA	AGCAGCCTGC	AGCGCAAGAA
361	GCCACCCTGG	CTAAAGCTGG	ACATTCCCTC	тесевтессс	CTGACGGCAG AAGAGCCCAG	AAGAGCCCAG
421	CTTCCTGCAG	CCCCTGAGGC	GACAGGCTTT	CCTGAGGAGT	GTGAGTATGC	CAGCCGAGAC
481	AGCCCACATC	TCTTCACCCC	ACCATGAGCT	<del>ವಿದ್ಯಾಕ್ಕರಿಕ್ಕಾರಿಕ್</del>	GTGCTGCAAC	GCCAGACGTC
541	CATCACACAG		ACCATCCGCA GGGGGACCGC	CGACTGGTTT	GGAGTGAGCA	AGGACAGTGA
601	CAGCACCCAG	AAATGGCAGC	GCAAGAGCAT	CCGTCACTGC	AGCCAGCGCT	ACGGGAAGCT
661	GAAGCCCCAG	GTCCTCCGGG	AGCTGGACCT	GCCCAGCCAG GACAACGIGI	GACAACGTGT	CGCTGACCAG
721	CACCGAGACG	CCACCCCCAC	TCTACGTGGG	GCCATGCCAG CTGGGCATGC	CTGGGCATGC	AGAAGATCAT
781	AGACCCCCTG	AGACCCCTG GCCCGTGGCC GTGCCTTCCG	GTGCCTTCCG	TGTGGCAGAT	GACACTGCGG AAGGCCTGAG	AAGGCCTGAG
841	TGCCCCACAC	ACTCCCGTCA CGCCGGGTGC	ದತ್ತದಾರವಾದ	TGCCTCCTC	TGCTCCTTCT	CCAGCTCCCG
901	CTCAGGTTTC	CACCGGCTCC	ອລອອລອອລອລ	CAAGCGAGAG	TCGGTGGCCA /	AGATGAGCTT
961	ವಾಕ್ತಾಕ್ಷ	GCAGCGCTGA	TGAAAGGCCG	CTCCGTTAGG (	GATGGCACCT	Tresceedec
1021	ACGCCGTCGA	ACGGCGTCGA AGCTTCACTC CAGCTAGCTT	CAGCTAGCTT	TCTGGAGGAG (	GACACAACTG 1	ATTTCCCCGA

TGAGCTGGAC ACATCCTTCT TTGCCCGGGA AGGTATCCTC CATGAAGAGC TGTCCACATA CCCGGATGAA GITITCGAGI CCCCATCGGA GGCAGCGCTA AAGGACTGGG AGAAGGCACC GGAGCAGGCG GACCTCACCG GCGGGCCCT GGACCGCAGC GAGCTTGAGC GCAGCCACCT GAIGCIGCCC TIGGAGCGAG GCIGGCGGAA GCAGAAGGAG GGCGCCGCAG CCCCGCAGCC GCCAGCGTAT CGCGGIGCCG GIGCGCAAGC ICTICGCCCG GGAGAAGCGG CCGIAIGGGC IGGGCAIGGI GGGACGCTC ACCAACCGCA CCTACCGCAA GCGCATCGAC AGCTTCGTCA AGCGCCAGAT CGTCACCATC CTAGCCGTGT GCATCTATGG CATCGCGCCC GTGGGCTTCT CGCAGCATGA GAAGCACTCC GCCTGCTGCG TGCGCAACGA CAGGTCGGGC TGCGTGCAGA CCTCGGAGGA CGAGGACAIG GACGACACA GGCCCTICII CACCIACIGG CITACCIICG IGCACICGCI GACGGIGGAC ICGGIGCIGC GGAACCGCGG GGICTACGAG AACGICAAGI ACGIGCAGCA GGAGAACTIC IGGAICGGGC CCAGCICGGA GGCCCICAIC CACCIGGGCG CCAAGIIIIIC GCCCTGCATG CGCCAGGACC CGCAGGTGCA CAGCTTCATT CGCTCGGCGC GCGAGCGCGA GGAGTGCTCG TCCACGCTGG CAGTGTGGGT GAAGTGGCCC ATCCATCCCA GCGCCCCAGA GCTIGCGGGC CACAAGAGAC AGTITGGCTC TGICTGCCAC CAGGAICCCA GGGIGIGIGA TGAGCCCTCC TCCGAAGACC CTCATGAGTG GCCAGAAGAC ATCACCAAGT GGCCGATCTG CACCAAAAAC AGCGCTGGGA ACCACCAA CCATCCCCAC ATGGACTGTG TCATCACAGG CTICAIGAGG GGCTACTICC AIGAGGAGGC CACGCICIGC ICICAGGIGC ACTGCAIGGA ACGGCCCTGC TGCATTGGCA CCAAGGGCAG GTGTGAGATC ACCTCCCGGG AGTACTGTGA CAAGGTGCGG CTCCGACAGG AGGTGGTGAG CACCGCGGGG CCGCGACGGG 1081 1141 1201 1261 1321 1381 1441 1501 1561 1621 1741 1681 1801 1921 1981 1861 2101 2161

TGATGTGTGT GGGCTCCTGC CTTTTCTCAA CCCCGAGGTG CCTGACCAGT TCTACCGCCT CICITCCIGC ACGCCGGGAT CITGCACTGC CTGGTGCTA TCTGCTTCCA GGCAGGCTGG CACCGCATAG CCATCATCTA CCTGCTGAGT GGTGTCACCG GCAACCTGGC CAGTGCCATC TTCCTGCCAT ACCGAGCAGA GGIGGGICCI GCIGGCICCC AGIICGGCAI CCIGGCCIGC CICIICGIGG AGCICIICCA GAGCTGGCAG ATCCTGGCGC GGCCCTGGCG TGCCTTCTTC AAGCTGCTGG CTGTGGTGCT TGGCCTGGTG GICCTCTTCT ACGTCTAICC TGTCCGCTGT GAGTGGTGTG AGTTCCTCAC CGCTCCTGAA GACCCAGAGG ATCTCGAGCA CCACCACCAC CACCACTAAT GTTAATTAAG CTICCICIIC ACCIIIGGGC IGCIGCCGIG GAIIGACAAC ITIGCCCCACA ICICGGGGII GCAAGTTCGA GCCTCCTGGC CTGCATCCCC TTCACTGACA AGTTCTGTGA GAAGTACGAA CTGGACGCTC AGCTCCACAT TCGAAGCTIG CGGCCGCACA GCIGIAIACA CGIGCAAGCC AGCCAGAACI TIGGGCGTIG TAATCATAGT CATAATCAAT ACTCCTGACT GCGTTAGCAA ITTAACTGTG ATAAACTACC GCATTAAAGC TATTCGATGA TAAGCTGTCA AACATGATAA TTCTTGAAGA CGAAAGGGCC TAGGCTGATA AAACAGAATT TGCCTGGCGG CAGTAGCGCG GTGGTCCCAC CTGACCCCAT GCCGAACTCA GAAGTGAAAC GCCGTAGCGC CGATGGTAGT GTGGGGGTCTC CCCATGCGAG AGTAGGGAAC TGCCAGGCAT CAAATAAAAC GAAAGGCTCA GTCGAAAGAC TGGGCCTTTC GITTTAICIG TIGITIGICG GIGAACGCIC ICCIGAGIAG GACAAAICCG CATCAGTGGC CTCTTCCTCT CCTTCGCCTT CTTGCCCTAC ATCAGCTTTG CCTGTACCGG AAACGCTGCC AGATCATCAT CTTTCAGGTG GTCTTCCTGG CTGCGGGACC TGGAGAAGCT GIGGCIATCC GATGACTGTC CGATACGCGT 2401 2461 2521 2581 2641 2701 2761 2821 2881 2941 3001 3061 3301 3121 3181 3241

TATTAATTGT TGCCGGGAAG CTAGAGTAAG TAGTTCGCCA GTTAATAGTT TGCGCAACGT	4441 TA
GCCAGCCGGA AGGGCCGAGC GCAGAAGTGG TCCTGCAACT TTATCCGCCT CCATCCAGTC	4381 GC
TGCTGCAATG ATACCGCGAG ACCCACGCTC ACCGGCTCCA GATTTATCAG CAATAAACCA	4321 TG
TGCCTGACTC CCCGTCGTGT AGATAACTAC GATACGGGAG GGCTTACCAT CTGGCCCCAG	4261 TG
CCAATGCTTA ATCAGTGAGG CACCTATCTC AGCGATCTGT CTATTTCGTT CATCCATAGT	4201 CC
TTAAAAATGA AGTTTTAAAT CAATCTAAAG TATATATGAG TAAACTTGGT CTGACAGTTA	4141 TT
TITCIGGCGG CACGAIGGCA IGAGATIAIC AAAAAGGAIC IICACCIAGA ICCIITIAAA	. 4081 TT
AAAATGAGCT GATTTAACAA AAATTTAACG CGAATTTTAA CAAAATATTA ACGTTTACAA	4021 AA
CTAICICGGI CIAIICTIII GAITIATAAG GGAITITGCC GAITICGGCC TAITGGIIAA	3961 CT
CGTIGGAGIC CACGIICIII AAIAGIGGAC ICTIGIICCA AACIGGAACA ACACICAACC	3901 CG
ATTAGGGTGA TGGTTCACGT AGTGGGCCAT CGCCCTGATA GACGGTTTTT CGCCCTTTGA	3841 AT
GGGGGCTCCC TTTAGGGTTC CGAFTTAGTG CTTTACGGCA CCTCGACCCC AAAAAACTTG	3781 GG
TCGCTTTCTT CCCTTCCTTT CTCGCCACGT TCGCCGGCTT TCCCCGTCAA GCTCTAAATC	3721 TC
GIGIGGIGGI IACGCGCAGC GIGACCGCIA CACTIGCCAG CGCCCTAGCG CCCGCTCCTI	3661 GT
GGAACTATAT CCGGATTGGC GAATGGGACG CGCCCTGTAG CGGCGCATTA AGCGCGGCGG	3601 GG
TAACTAGCAT AACCCCTTGG GGCCTCTAAA CGGGTCTTGA GGGGTTTTTT GCTGAAAGGA	3541 TA
TITCTACAAA CTCTTTTGTT TATTTTTTTA AATACAITCA AATATGTATC CGCTGAGCAA	3481 TT
CCATAAACTG CCAGGCATCA AATTAAGCAG AAGGCCATCC TGACGGATGG CCTTTTTGCG	3421 .CC
CCGGGAGCGG ATTTGAACGT TGCGAAGCAA CGGCCCGGAG GGTGGCGGGC AGGACGCCCG	3361 CC

TGTTGCCATT GCTACAGGCA TCGTGGTGTC ACGCTCGTCG TTTGGTATGG CTTCATTCAG TGAGATCCAG AAAAAGCGGT TATCACTCAT CGAGTTGCTC TICTGGGTGA GCAAAAACAG GAAGGCAAAA TGCCGCAAAA AAGGGAATAA GGGCGACACG GAAATGITGA ATACTCATAC ICTICCITIT ICAAICAIGA CCAAAAICCC ITAACGIGAG GGTTATGGCA GCACTGCATA ATTCTCTTAC TGTCATGCCA TCCGTAAGAT GCTTTTCTGT TTGCCCGGCG TCAATACGGG ATAATACCGC GCCACATAGC AGAACTTTAA AAGTGCTCAT TTCGATGTAA CCCACTCGTG CACCCAACTG ATCTTCAGCA TCTTTTACTT TCACCAGCGT TITICGITCC ACTGAGCGIC AGACCCCGIA GAAAAGAICA AAGGAICTIC IIGAGAICCI TITITICIGC GCGIAAICIG CIGCIIGCAA ACAAAAAAC CACCGCIACC AGCGGIGGII TGTITGCCGG ATCAAGAGCT ACCAACTCTT TTTCCGAAGG TAACTGGCTT CAGCAGAGCG CAAGAACTCT GTAGCACCGC CTACATACCT CGCTCTGCTA ATCCTGTTAC CAGTGGCTGC TGCCAGTGGC GGCGCAGCGG TCGGGCTGAA CGGGGGTTC GTGCACACAG CCCAGCTTGG AGCGAACGAC CTACACCGAA CTGAGATACC TACAGCGTGA GCTATGAGAA AGCGCCACGC TTCCCGAAGG GAGAAAGGCG GACAGGTATC CGGTAAGCGG CAGGGTCGGA ACAGGAGAGC GCACGAGGGA GCTTCCAGGG CTCCGGTTCC CAACGATCAA GGCGAGTTAC ATGATCCCCC ATGTTGTGCA TAGCTCCTTC GGTCCTCCGA TCGTTGTCAG AAGTAAGTTG GCCGCAGTGT GACTGGTGAG TACTCAACCA AGTCATTCTG AGAATAGTGT ATGCGGCGAC CATTGGAAAA CGTTCTTCGG GGCGAAAACT CTCAAGGATC TTACCGCTGT CAGATACCAA ATACTGTCCT TCTAGTGTAG CCGTAGTTAG GCCACCACTT TACCGGATAA GATAAGTCGT GTCTTACCGG GTTGGACTCA AGACGATAGT 4501 4561 4621 4681 4741 4801 4861 4921 4981 5041 5101 5161 5281 5341 5401 5461 5521 5581 5221

GAAAT

6181

	AACGICCCGC	TGCGGCGACG ACCGGTGAAT TGTGAGCGCT CACAATTCTC GTGACATCAT AACGTCCCGC	CACAATTCTC	TGTGAGCGCT	ACCGGTGAAT	TGCGGCGACG	6121
	CAGTCATAAG	GACCCAGAGC GCTGCCGGCA CCTGTCCTAC GAGTTGCATG ATAAAGAAGA CAGTCATAAG	GAGTIGCAIG	CCTGTCCTAC	GCTGCCGGCA	GACCCAGAGC	1909
-	CGCCGAAAAT	TACCGCAAGC GACAGGCCGA TCATCGTCGC GCTCCAGCGA AAGCGGTCCT CGCCGAAAAT	GCTCCAGCGA	TCATCGTCGC	GACAGGCCGA	TACCGCAAGC	6001
	AGATTCCGAA	GAAACGTTTG GTGGCGGGAC CAGTGACGAA GGCTTGAGCG AGGGCGTGCA AGATTCCGAA	GGCTTGAGCG	CAGTGACGAA	GTGGCGGGAC	GAAACGTTTG	5941
	GCTTCTCGCC	ACGACCGAGC GCAGCGAGTC AGTGAGCGAG GAAGCCGGCG ATAATGGCCT GCTTCTCGCC	GAAGCCGGCG	AGTGAGCGAG	GCAGCGAGTC	ACGACCGAGC	5881
	CCGCAGCCGA	GAITCTGIGG AIAACCGIAI TACCGCCIIT GAGIGAGCIG AIACCGCICG CCGCAGCCGA	GAGTGAGCTG	TACCGCCTTT	ATAACCGTAT	GATTCTGTGG	5821
	GTTAICCCCT	TTACGGTICC IGGCCTTITG CIGGCCTTIT GCICACAIGI ICTITCCIGC GITAICCCCI	GCTCACATGT	CTGGCCTTTT	TGGCCTTTTG	TIACGGITCC	5761
	CGCGGCCTTT	TITITGEGAT GCTCGTCAGG GGGGCGGAGC CTATGGAAAA ACGCCAGCAA CGCGGCCTTT	CTATGGAAAA	GGGGCGGAGC	GCTCGTCAGG	TTTTTGTGAT	5701
	TGAGCGTCGA	ACCICIGACI	GGAAACGCCT GGTATCTTTA TAGTCCTGTC GGGTTTCGCC ACCTCTGACT TGAGCGTCGA	TAGTCCTGTC	GGTATCTTTA	GGAAACGCCT	5641

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'IG. 31, (SEQ ID NO:68) Coding region fo	
FIG. 31, (SEQ ID NO:68) Coding region for the N terminus 400 as of ICT1024: 314-1515	

CACTATAGGG GAATTGTGAG CGGATAACAA TTCCCCTCTA GACTTACAAT	GGCCICTICG	GGTAACGCCA	ATTGGCTAGC	GGGAGCTCGT	AGCGCAAGAA	AAGAGCCCAG	CAGCCGAGAC	GTGCTGCAAC GCCAGACGTC	CGACTGGTTT GGAGTGAGCA AGGACAGTGA	CCGTCACTGC AGCCAGCGCT ACGGGAAGCT	CGCTGACCAG	AGAAGATCAT	GACACTGCGG AAGGCCTGAG	CCAGCTCCCG	AGATGAGCTT	TTCGCCGGGC	ATTTCCCCGA
TTCCCCTCTA	TGGGAAGGGC GATCGGTACG	GATTAAGTTG	AGAGATCTTG	GCGATATCCC	AGCAGCCTGC	CTGACGGCAG	GTGAGTATGC		GGAGTGAGCA	AGCCAGCGCT	GACAACGTGT	CTGGGCATGC		TGCTCCTTCT	TCGGTGGCCA	GATGGCACCT	GACACAACTG
CGGATAACAA	TGGGAAGGGC	CGGTGGGTGC GCTGCAAGGC	ACGCCCAGCG	ATATACCATG	GGACAGCACG	receereccc	CCTGAGGAGT	ອວວອອວອອວວ			GCCCAGCCAG	GCCATGCCAG	TGTGGCAGAT	TGCCTCCTC	CAAGCGAGAG	CTCCGTTAGG GATGGCACCT	TCTGGAGGAG GACACAACTG
GAATTGTGAG	GCGCAACTGT	CGGTGGGTGC	TTGTAAAACG	TAAGAAGGAG	AGGCCCGCAG	CTAAAGCTGG ACATTCCCTC	CCCCTGAGGC GACAGGCTTT	ACCATGAGCT	GGGGGACCGC	GCAAGAGCAT	AGCTGGACCT	TCTACGTGGG	GTGCCTTCCG	CGCCGGGTGC	ຄວອຄວຄຄວຄວ	TGAAAGGCCG	CAGCTAGCTT
CACTATAGGG	CATTCAGGCT	CTATTACGCC AGCTTGCGAA	GGATTCTCCC AGTCACGACG	TGTTTAACTT	TCCATGAGTG	CTAAAGCTGG	CCCCTGAGGC	TCTTCACCCC ACCATGAGCT	ACCATCCGCA GGGGGACCGC	AAATGGCAGC	Greereege	משממממשמ	cccereecc	ACTCCCGTCA	CACCGGCTCC	GCAGCGCTGA	AGCTTCACTC
TAATACGACT	TTCCATTCGC	CTATTACGCC	GGATTCTCCC	AGAATAATTT	GGATCCGAAT	GCCACCCTGG	CTTCCTGCAG	AGCCCACATC	CATCACACAG	CAGCACCCAG AAATGGCAGC GCAAGAGCAT	GAAGCCCCAG GTCCTCCGGG AGCTGGACCT	CACCGAGACG	AGACCCCCTG	TGCCCCACAC	CTCAGGTTTC	ಎರಿಕಿರಿಕಿಕಿರಿ	ACGGCGTCGA AGCTTCACTC
Н	61	121	181	241	301	361	421	481	541	601	661	721	781	841	901	196	1021

TGAGCIGGAC ACAICCTICI TIGCCCGGGA AGGIAICCIC CAIGAAGAGC IGICCACAIA CCCGGATGAA GITITCGAGI CCCCATCGGA GGCAGCGCTA AAGGACTGGG AGAAGGCACC GGAGCAGGCG GACCTCACCG GCGGGCCCT GGACCGCAGC GAGCTTGAGC GCAGCCACCT GATGCTGCCC TTGGAGCGAG GCTGGCGGAA GCAGAAGGAG GGCGCCGCAG CCCCGCAGCC GCCAGCGTAT CGAGGACATG GACATCGATA CGCGTTCGAA GCTTGCGGCC GCACAGCTGT ATACACGTGC AGCAATTTAA CTGTGATAAA CTACCGCATT AAAGCTATTC GATGATAAGC TGTCAAACAT TGGGCATGGT GGGACGCTC ACCAACCGCA CCTACCGCAA GCGCATCGAC AGCTTCGTCA AGCGCCAGAT AAGCCAGCCA GAACTCGCTC CTGAAGACCC AGAGGATCTC GAGCACCACC ACCACCACA CTAATGTTAA TTAAGTTGGG CGTTGTAATC ATAGTCATAA TCAATACTCC TGACTGCGTT GATAATICIT GAAGACGAAA GGGCCTAGGC TGATAAAACA GAATTIGCCT GGCGGCAGTA GCGCGGTGGT CCCACCTGAC CCCATGCCGA ACTCAGAAGT GAAACGCCGT AGCGCCGATG GTAGTGTGGG GTCTCCCCAT GCGAGAGTAG GGAACTGCCA GGCATCAAAT AAAACGAAAG GCTCAGTCGA AAGACTGGGC CTTTCGTTTT ATCTGTTGTT TGTCGGTGAA CGCTCTCCTG AGTAGGACAA ATCCGCCGGG AGCGGATTTG AACGTTGCGA AGCAACGGCC CGGAGGGTGG CGGGCAGGAC GCCCGCCATA AACTGCCAGG CATCAAATTA AGCAGAAGGC CATCCTGACG GAIGGCCTTT TIGCGTITCT ACAAACICTT TIGITIAITT ITCIAAAIAC AITCAAAIAI GTATCCGCTG AGCATAACT AGCATAACCC CTTGGGGCCT CTAAACGGGT CTTGAGGGGT CAAGGTGCGG CTCCGACAGG AGGTGGTGAG CACCGCGGGG CCGCGACGGG CGCGGTGCCG GTGCGCAAGC TCTTCGCCCG GGAGAAGCGG CCGTATGGGC 1081 1141 1261 1381 1441 1501 1561 1741 1321 1621 1681 1801 1861 1981 2041 2161 1921 2101

TCA CTCATGGTTA TGGCAGCACT GCATAATTCT CTTACTGTCA TGCCATCCGT	AGTGTTATCA	3301
AAA GCGGTTAGCT CCTTCGGTCC TCCGATCGTT GTCAGAAGTA AGTTGGCCGC	GTGCAAAAAA	3241
TCA ITCAGCICCG GIICCCAACG AICAAGGCGA GIIACAIGAI CCCCCAIGII	TATGGCTTCA	3181
CGC AACGTIGITG CCATTGCTAC AGGCATCGTG GTGTCACGCT CGTCGTTTGG	TAGITIGCGC	3121
AIC CAGICIAITA AITGIIGCCG GGAAGCIAGA GIAAGIAGII CGCCAGIIAA	CGCCTCCATC	3061
ATA AACCAGCCAG CCGGAAGGGC CGAGCGCAGA AGTGGTCCTG CAACTTTATC	ATCAGCAATA	3001
GGC CCCAGTGCTG CAATGATACC GCGAGACCCA CGCTCACCGG CTCCAGATTT	ACCATCIGGC	2941
TCC ATAGTTGCCT GACTCCCGT CGTGTAGATA ACTACGATAC GGGAGGGCTT	TCGTTCATCC	2881
GAC AGTTACCAAT GCTTAATCAG TGAGGCACCT ATCTCAGCGA TCTGTCTATT	TTGGTCTGAC	2821
CTT TTAAATTAAA AATGAAGTTT TAAATCAATC TAAAGTATAT ATGAGTAAAC	CTAGATCCTT	2761
GIT TACAATITICT GGCGCACGA TGGCATGAGA TTAICAAAAA GGATCTTCAC	TATTAACGTT	2701
ITTG GTTAAAAAT GAGCTGATTT AACAAAATT TAACGCGAAT TTTAACAAAA	CGGCCTATTG	2641
ACT CAACCCTATC TCGGTCTATT CTTTTGATTT ATAAGGGATT TTGCCGATTT	GAACAACACT	2581
SCCC TITGACGITG GAGICCACGI ICTITAATAG IGGACICITG IICCAAACIG	TTTTTCGCCC	2521
AAAA ACTTGATTAG GGTGATGGTT CACGTAGTGG GCCATCGCCC TGATAGACGG	ACCCCAAAAA	2461
TICT AAATCGGGGG CTCCCTTTAG GGTTCCGAIT TAGTGCTTTA CGGCACCTCG	GTCAAGCTCT	2401
des rectrices ricricetr cerrese exerrese secrirese	TAGCGCCCGC	2341
SCGC GGCGGGTGTG GTGGTTACGC GCAGCGTGAC CGCTACACTT GCCAGCGCCC	CATTAAGCGC	2281
TTTTTGCTGA AAGGAGGAAC TATATCCGGA TTGGCGAATG GGACGCGCCC TGTAGCGGCG	TTTTGCTG	2221

AAGATGCTTT TCTGTGACTG GTGAGTACTC AACCAAGTCA TTCTGAGAAT AGTGTATGCG TGCTCTTGCC CGGCGTCAAT ACGGGATAAT ACCGCGCCAC ATAGCAGAAC CICATCATIG GAAAACGIIC IICGGGGGGA AAACICICAA GGAICIIACC AATAAGGGCG ACACGGAAAT GTTGAATACT CATACTCTTC CTTTTTCAAT CATGACCAAA GCTGTTGAGA TCCAGITCGA TGTAACCCAC TCGTGCACCC AACTGATCTT CAGCATCTTT TACTITCACC AGCGTTICTG GGTGAGCAAA AACAGGAAGG CAAAATGCCG CAAAAAAGGG TCTTCTTGAG ATCCTTTTTT TCTGCGCGTA ATCTGCTGCT TGCAAACAAA AAAACCACCG ATCCCTTAAC GTGAGTTTTC GTTCCACTGA GCGTCAGACC CCGTAGAAAA GATCAAAGGA GGCTTCAGCA GAGCGCAGAT ACCAAATACT GTCCTTCTAG TGTAGCCGTA GTTAGGCCAC GITACCAGIG GAAGGTAACT GCTGCTGCCA GTGGCGATAA GTCGTGTTT ACCGGGTTGG ACTCAAGACG ATAGTTACCG GATAAGGCGC AGCGGTCGGG CTGAACGGGG GGTTCGTGCA CACAGCCCAG CTTGGAGCGA ACGACCTACA CCGAACTGAG ATACCTACAG CGTGAGCTAT GAGAAAGCGC CACGCTTCCC GAAGGGAGAA AGGCGGACAG GTATCCGGTA AGCGGCAGGG TCGGAACAGG AGAGCGCACG AGGGAGCTIC CAGGGGGAAA CGCCIGGIAI CITIAIAGIC CIGICGGGII ICGCCACCIC CCIGCGITAI CCCCIGAITC IGIGGAIAAC CGIAITACCG CCITIGAGIG AGCIGAIACC TGACTIGAGC GICGAITITI GIGAIGCICG ICAGGGGGG GGAGCCIAIG GAAAAACGCC AGCAACGCGG CCTITITACG GTICCTGGCC TTTTGCTGGC CTTTTGCTCA CATGITCTTT CTCTTTTCC CACTICAAGA ACTCIGIAGC ACCGCCIACA IACCICGCIC IGCIAAICCI CTACCAGCGG IGGTITGITT GCCGGAICAA GAGCTACCAA TTTAAAAGTG GCGACCGAGT 3361 3421 3541 3601 3721 3781 3841 3901 3961 4021 4141 4201 4321 4081 4441

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FIG. 32, (SEQ ID NO 69) Coding region for
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rcegrace eeccrcri	TTAAGTTG GGTAACGCCA	AGATCTTG ATTGGCTAGC	ATAICCC GGGAGCICGI	GAGCGCG AGAAGCACTC	TCGGAGG AGGAGTGCTC	GCCCCAG AGCTTGCGGG	GTGTGTG ATGAGCCCTC	CCGATCT GCACCAAAAA	ATCACAG GACGGCCCTG	TACTGIG ACTICAIGAG	TGCATGG ATGATGTGTG	TACCGCC TGTGGCTATC	TGCTTCC AGATGACTGT	ATCATCT ACCTGCTGAG	CGAGCAG AGGTGGGTCC	GAGCTCTTCC AGAGCTGGCA
GAI	GAI	AGA	වුටුව	) (G	ACC	AGC	AGG	TGG	GIC	GAG	CAC	TTC	ATC	3007	FAC	3AG(
	GCTGCAAGGC	ACGGCCAGCG	ATATACCATG	TCGCTCGGCG	CTGCGTGCAG	CATCCATCCC		CATCACCAAG	CATGGACTGT	CACCTCCCGG	CTCTCAGGTG	GCCTGACCAG	CCIGGIGICC	GCACCGCATA	CTTCCTGCCA	CCTCTTCGTG (
GCGCAACTGT	CGGTGGGTGC	TTGTAAAACG	TAAGAAGGAG		ACAGGTCGGG	TGAAGTGGCC	CTGTCTGCCA	GGCCAGAAGA	ACCATCCCCA	GGTGTGAGAT	CCACGCTCTG	ACCCCGAGGT	TCTTGCACTG	reccaeecre		rccreeccre
	AGCTTGCGAA	AGTCACGACG	TGTTTAACTT	TCCCAGGTGC	GTGCGCAACG	GCAGTGTGGG	CAGTTTGGCT	CCTCATGAGT	AACCACACCA	ACCAAGGGCA	CATGAGGAGG	CCTTTTCTCA	CACGCCGGGA	CTGGAGAAGC	GGCAACCTGG	CAGTICGGCA ICCIGGCCIG
TTCCATTCGC	CTATTACGCC	GGATTCTCC	AGAATAATTT	GGATCCGAAT	CGCCTGCTGC	GTCCACGCTG	CCACAAGAGA	CTCCGAAGAC	CAGCGCTGGG	CTGCATTGGC	GGGCTACTTC	TGGGCTCCTG	CCTCTTCCTG	CCTGCGGGAC	TGGTGTCACC	TGCTGGCTCC
61	121	181	241	301	361	421	481	541	601	199	721	781	841	901	961	1021
	61 TTCCATTCGC CATTCAGGCT GCGCAACTGT TGGGAAGGGC GATCGGTACG GGCCTCTTCG	TICCATICGC CATICAGGCT GCGCAACTGT TGGGAAGGGC GAICGGTACG CTAITACGCC AGCTIGCGAA CGGTGGGTGC GCTGCAAGGC GATTAAGTTG	TICCALICGC CATICAGGCT GCGCAACTGT TGGGAAGGGC GAICGGTACG CTATTACGCC AGCTIGCGAA CGGTGGGTGC GCTGCAAGGC GAITAAGTIG GGAITCICCC AGTCACGACG ITGTAAAACG ACGGCCAGCG AGAGAICTTG	TICCATICGC CATTCAGGCT GCGCAACTGT TGGGAAGGGC GAICGGTACG CTATTACGCC AGCTTGCGAA CGGTGGGTGC GCTGCAAGGC GATTAAGTTG GGATTCTCCC AGTCACGACG TTGTAAAACG ACGGCCAGCG AGAGATCTTG AGAATAATTT TGTTTAACTT TAAGAAGGAG ATATACCATG GCGATAICCC	TICCATICGC CATICAGGCT GCGCAACTGT TGGGAAGGGC GAICGGTACG CTATTACGCC AGCTTGCGAA CGGTGGGTGC GCTGCAAGGC GAITAAGTTG GGATTCTCCC AGTCACGACG TTGTAAAACG ACGGCCAGCG AGAGATCTTG AGAATAATTT TGTTTAACTTT TAAGAAGGAG ATATACCATG GCGATATCCC GGATCCGAAT TCCCAGGTGC ACAGCTTCAT TCGCTCGGCG CGCGAGCGCG	TICCATICGC CATICAGGCT GCGCAACTGT TGGGAAGGGC GAICGGTACG CTATTACGCC AGCTTGCGAA CGGTGGGTGC GCTGCAAGGC GAITAAGTTG GGATTCTCCC AGTCACGACG TTGTAAAACG ACGCCCAGCG AGAGATCTTG AGAATAATTT TGTTTAACTT TAAGAAGGAG ATATACCATG GCGATATCCC GGATCCGAAT TCCCAGGTGC ACAGCTTCAT TCGCTCGGCG CGCGAGCGCG CGCCTGCTGC GTGCGAACG ACAGGTCGGG CTGCGTGCCAG ACCTCGGAGG	TTCCATTCGC CATTCAGGCT GCGCAACTGT TGGGAAGGGC GATCGGTACG CTATTACGCC AGCTTGCGAA CGGTGGGTGC GCTGCAAGGC GATTAAGTTG GGATTCTCCC AGTCACGACG TTGTAAAACG ACGGCCAGCG AGAGATCTTG AGAATAATTT TGTTTAACTT TAAGAAGGAG ATATACCATG GCGATATCCC GGATCCGAAT TCCCAGGTGC ACAGCTTCAT TCGCTCGGCG GCCGAGCGCG CGCCTGCTGC GTGCGCAACG ACAGGTCGGC CTGCGTGCAG ACCTCGGAGG GTCCACGCTG GCAGTGTGG TGAAGTGGCC CATCCATCCC AGCGCCCAG	TTCCATTCGC CATTCAGGCT GCGCAACTGT TGGGAAGGGC GATCGGTACG CTATTACGCC AGCTTGCGAA CGGTGGGTGC GCTGCAAGGC GATTAAGTTG GGATCTCCC AGTCACGACG TTGTAAAACG ACGGCCAGCG AGAGATCTTG AGAATAATTT TGTTTAACTTT TAAGAAGGAG ATATACCATG GCGATATCCC GGATCCGAAT TCCCAGGTGC ACAGCTTCAT TCGCTCGGCG CGCGAGCGCG CGCCTGCTGC GTGCGCAACG ACAGGTCGGG CTGCGTGCCA ACCTCCGAAGG CGCCTGCTGC GTGCGCAACG ACAGGTCGCC CATCCATCCC AGGGTGTGTG CCACAAGAGA CAGTTTGGCT CTGTCTGCCA CCAGGATCCC AGGGTGTGTG	TTCCATTCGC CATTCAGGCT GCGCAACTGT TGGGAAGGGC GATCGGTACG CTATTACGCC AGCTTGCGAA CGGTGGGTGC GCTGCAAGGC GATTAAGTTG GGATTCTCCC AGTCACGACG TTGTAAAACG ACGGCCAGCG AGAGATCTTG AGAATAATTT TGTTTAACTT TAAGAAGGAG ATATACCATG GCGATATCCC GGATCCGAAT TCCCAGGTGC ACAGCTTCAT TCGCTCGGCG CGCGAGCCGG CGCCTGCTGC GTGCGCAACG ACAGGTCGGG CTGCGTGCAG ACCTCGGAGG CGCCTGCTGC GTGCGCAACG TGAAGTGGCC CATCCATCCC AGCGCCCCAG GTCCACAGGAG CAGTTTGGCT CTGTCTGCCA CCAGGATCCC CCACAAGAGA CAGTTTGGCT CTGTCTGCCA CCAGGATCTC	TTCCATTCGC CATTCAGGCT GCGCAACTGT TGGGAAGGGC GATCGGTACG CTATTACGCC AGTTGCGAA CGGTGGGTGC GCTGCAAGGC GATTAAGTTG GGATCTCCC AGTCACGACG TTGTAAAACG ACGGCCAGCG AGAGATCTTG AGAATAATTT TGTTTAACTT TAAGAAGGAG ATATACCATG GCGATATCCC GGATCCGAAT TCCCAGGTGC ACAGCTTCAT TCGCTCGGCG CGCGAGCGCG CGCCTGCTGC GTGCGCAACG ACAGGTTCAG CTGCCTCGGCG CGCGAGCGCG CGCCTGCTGC GTGCGCAACG ACAGGTTCGCG CTGCCTCCACG ACCCCCCAG CCCCCAAGGAG CAGTTTGGCT CTGTCTGCCA CCAGGATCCC CCACAAGAGA CAGTTTGGCT CTGTCTGCCA CCAGGATCCC CCACAAGAGA CAGTTTGGCT CTGTCTGCCA CCAGGATCTC CCACAAGAGA CAGTTTGGCT CTGTCTGCCA CATGGACTGT GTCATCACAG	TTCCATTCGC CATTCAGGCT GCGCAACTGT TGGGAAGGGC GATCGGTACG CTATTACGCC AGCTTGCGAA CGGTGGGTGC GCTGCAAGGC GATTAAGTTG GGATTCTCCC AGTCACGACG TTGTAAACG ACGGCCAGCG AGAGATCTTG AGAATAATTT TGTTTAACTT TAAGAAGGAG ATATACCATG GCGATATCCC GGATCCGAAT TCCCAGGTGC ACAGGTTCAT TCGCTCGGCG CGCGAGCGCG CGCCTGCTGC GTGCGCAACG ACAGGTTCAT TCGCTCGGCG CGCGGCGCG CGCCTGCTGC GTGCGCAACG ACAGGTCGCG CTGCCTGCTCC AGCGCCCCAG CCCCACAGAGA CAGTTTGGCT CTGTCTGCC CATCCATCCC AGGGTGTGTG CCACAAGAGA CAGTTTGGCT CTGTCTGCCA CCAGGATCCC CCACAAGAGA CACTTGGCT GGCCAGAAGA CATCACCAAG TGGCCGATCT CTCCGAAGAC CCTCATGAGT GGCCAGAAGA CATCACCCAAG TGCCCATCAG CTGCATTGGC ACCAAGGGCA GGTGTGAAT CACCTCCCGG GAGTACTGTG	TTCCATTCGC CATTCAGGCT GCGCAACTGT TGGGAAGGGC GATCGGTACG CTATTACGCC AGCTTGCGAA CGGTGGGTGC GCTGCAAGGC GATTAAGTTG GGATTCTCCC AGTCACGACG TTGTAAAACG ACGGCCAGCG AGAGATCTTG AGAATAATTT TGTTTAACTT TAAGAAGGAG ATATACCATG GCGATATCCC GGATCCGAAT TCCCAGGTGC ACAGCTTCAT TCGCTCGGCG CGCGAGCGCCG CGCCTGCTGC GTGCGCAACG ACAGGTTCAT TCGCTCGGCG CGCGAGCGCCG CGCCTGCTGC GTGCGCAACG ACAGGTTCGCC CATCCATCCC AGCGCCCCAG GTCCACGCTG GCAGTGTGGC TGAAGTGGCC CATCCATCCC AGCGTCTTGTG CTCCAAGAGA CAGTTTGGCT CTGTCTGCCA CCAGGATCTC CTCCGAAGAC CAGTTTGGCT CTGTCTGCCA CATCGACTGT GTCATCACAG CTCCGAAGAC ACCATCCCCA ACCATCCCCA CATCGACTGT GTCATCACAG CTGCATTGGC ACCAAGGACA CCATCCCCGG GAGTACTGTG CTGCATTGGC CATGAGGAGG CCACGCTCTG CTCCTCAGGTG CACTGCATGG	TTCCATTCGC CATTCAGGCT GCGCAACTGT TGGGAAGGGC GATCGGTACG CTATTACGCC AGCTTGCGAA CGGTGGGTGC GCTGCAAGGC GATTAAGTTG GGATTCTCCC AGTCACGACG TTGTAAAACG ACGGCCAGCG AGAGATCTTG AGAATAATTT TGTTTAACTT TAAGAAGGAG ATATACCATG GCGATATCCC GGATCCGAAT TCCCAGGTGC ACAGCTTCAT TCGCTCGGCG CGCGAGCGCG CGCCTGCTGC GTGCGCAACG ACAGCTCGCG CTGCGTGCAG ACCTCCGAACG TGAAGTTGGCC CATCCATCCC AGCGTCTGGG CTCCAAAGAGA CAGTTTGGCT CTGTCTGCCA CCAGGATCCC AGCGTGTGTG CTCCGAAGAGA CAGTTTGGCT CTGTCTGCCA CATCACCAAG TGGCCGATCT CTCCGAAGAG CACTATGGCT CTGTCTGCCA CATCACCAAG TGGCCGATCT CTGCATTGGC AACCAAGAGA ACCATCCCCA CATGGATTGTG CTGCATTGGC ACCAAGGAGA CCACGTTGAAGA TACTCAAGGTG CTGCATTGGC ACCAAGGAGG CCACGCTCTG CTCTCAAGGTG CTGCATTTGC ACCAAGGAGG CCACGCTCTG CTCTCAAGGTG TGGGCTTACTTC CATGAAGAGG CCACGCTCTG GCCTGACCAG TTCTACCGCC TGGGCTTCTTC CATGAAGAGG CCACGCTCTG GCCTGACCAG TTCTACCGCC	TTCCATTCGC CATTCAGGCT GCGCAACTGT TGGGAAGGGC GATCGGTACG CTATTACGCC AGCTTGCGAA CGGTGGGTGC GCTGCAAGGC GATTAAGTTG GGATTCTCCC AGTCACGACG TTGTAAAACG ACGGCCAGCG AGAGATCTTG AGAATAATTT TGTTTAACTT TAAGAAGGAG ATATACCATG GCGATATCCC GGATCCGAAT TCCCAGGTGC ACAGCTTCAT TCGCTCGGCG CGCGAGCGCG CGCCTGCTGC GTGCGCAACG ACAGGTTCAT TCGCTCGGCG CGCGAGCGCG CGCCTGCTGC GTGCGCAACG ACAGGTTCAT TCGCTCGGCG CGCGAGCCC CGCCTGCTGC GTGCGCAACG ACAGGTTCAT TCGCTCGGCG CGCGATCTCC CGCCTGCTGC GTGCGCAACG TGAAGTGGCC CATCCATCCC AGGGTCTGTG CCACAAGAGA CAGTTTGGCT CTGTCTGCCA CAGGGTCTTGTG CTCCGAAGAC CCTCATGAGT GGCCAGAAGA CATCACCAAG TGGCCGATCT CAGCGCTGGG AACCACACACA ACCATCCCCA CATCACAGGTG CACTGCATGGG TGGGCTACTTC CATGAGGAGG CCACGCTCTG CTCTCAGGTG TCTTACCGCC TGGGCTCCTG CCTTTTTCTCA ACCCCGAGGT GCCTGACCTGC CCTCTTCCTG CATTTCTCA ACCCCGAGGT CCTTCAAGGTG CACTGCTTCC ATCTGCTTCC A	TTCCATTCGC CALTCAGGCT GCGCAACTGT TGGGAAGGGC GATCGGTACG CTATTACGCC AGCTTGCGAA CGGTGGGTGC GCTGCAAGGC GATTAAGTTG GGATTCTCCC AGTCAGGTGC TTGTAAAACG ACGCCCAGG AGAGATCTTG AGAATAATTT TGTTTAACTT TAAGAAGGAG ATATACCATG GCGATATCCC GGATCCGAAT TCCCAGGTGC ACAGCTTCAT TCGCTCGGCG CGCGAGCGCG CGCCTGCTGC GTGCGCAACG ACAGGTTCAT TCGCTCGGCG CGCGAGCGCG CGCCTGCTGC GTGCGCAACG ACAGGTTCAT TCGCTCGGCG CGCGAGCGC CGCCTGCTGC GTGCGCAACG ACAGGTTCGC CATCCATCCC AGGGTGTTG CTCCGAAGAG CAGTTTGGCT CTGTCTGCCA CCAGGATCTTC CACCAGAGAC CCTCATGAGT GGCCAGAAGA CATCACCCAAG TGGCCCAAG CTCCGAAGAC CCTCATGAGT GGCCAGAAGA CATCACCCAAG GAGTACTGTG CTGCATTGGC ACCAAGGGCA GGTGTGAAGA CACCTCCAGGTG CACTGCATGTG GGGCTACTTC CATGAGGAGA CCACGCTTG CTCTCAGGTG CACTGCATCC CTGCATTGGC ACCAAGGGCA GGTGTGAAGT GCCTGACCCC CCTCCTGCGGGAC CTGTTCTCAA ACCCCCGAAGT GCCTGACCTC ATCTGCTTCC CCTGCGGGAC CTGCTGCACTG CCTGGTGTCC ATCTGCTTCC CCTGCGGGAC CTGCTGCACTG GCCTGCTGTCC ATCTGCTTCC CCTGCGGGAC CTGCTGCACTG GCCTGCTCTC ATCTGCTTCC CCTGCGGGAC CTGCTGCACTG GCCTGCTCCT ACCTGCTTCC ACCTGCTTCC ACCTGCTGTCT ACCTGCTGTTC ACCTGCTGTTC ACCTGCTGTTC ACCTGCTGTTC ACCTGCTTCCT ACCTGCTGTTC ACCTGCTTCCT ACCTGCTGTTC ACCTGCTTCT ACCTGCTGTTC ACCTGCTTCT ACCTGCTGTTC ACCTGCTTCT ACCTGCTGTTC ACCTGCTTCT ACCTTCTCT ACCTTCTCT ACCTTCTCTCT ACCTTCTCT ACCTTCTTCT AC	TTCCATTCGC CALTCAGGCT GCGCAACTGT TGGGAAGGGC GATCGGTACG CTATTACGCC AGTTCAGGA CGGTGGGTGC GCTGCAAGGC GATTAAGTTG AGAATAATTT TGTTTAACTT TAAGAAGGAG ATATACCATG GCGATATCCC GGATCCGAAT TCCCAGGTGC ACAGCTTCAT TCGCTCGGCG CGCGAGCGCG CGCCTGCTGC GTGCGCAACG ACAGCTCGCG CTTCCATCCC AGCGCCCCAG CCCCAAAGAGA CAGTTTGGCT CTGTCTGCCA CCTCCATCAG TGGCCCCAG CTCCGAAGAG CACTTTGGCT CTGTCTGCCA CATCGATCTG GTCCTCAGGTG CTCCGAAGAG CACTTTGACT CTGTCTGAAGA CATCCACAGG CTGCATTGGC ACCCACAGGC CATCCACAGG TGGCCGATCT CTGCATTGGC CCTCATGAGAG CCACGCTTGC CTTCAAGGTG CACTGCTTGG TGGGCTACTTC CATGAGAGG CCACGCTTG CTCTCAAGGTG CACTGCTTGC CCTGCTGCTGC CCTGTTCAA ACCCCGAGGT CTCTCAAGGTG CACTGCTTTCC CCTGCGGGAC CTGGAGAAGC CTTCTCAAGTG TACCGAGGGG CCTGCTGCCTG CCTGGTGCAA ACCTTCACAGTG CCTGGTTGCTTC CTGGGGTGTTCCTG CCTGGTGAAGA CTTCTGCTTCC CCTGCTGCGGAC CTGGAGAAGC CTGGAGGTTC ATCTGCTTTCC CCTGCTGCGGAC CTGGAGAAGC CTGCAACGCTG CCTGCTTACCGCC CCTGCTGCGGAC CTGGAGAAGC CTGCAACCCAA ACCTGCAACGCTG CTTCCTGCCA TACCGAGCAG TACCGAAGGAGG CCTGCTACCTGCCA TACCGAAGGAGG TTCCTGCCAA TACCGAAGGAG TTTCCTGCCA TACCGAAGGAG TTTCCTGCCA TACCGAAGGAGG TTTCCTGCCAA TACCGAAGGAGG TTCCTGCCAAGGAGG TTTCCTGCCAAG TACCCTAGAGAGG TTTCCTGCCAAG TACCCTAGCAAGG TTCCTGCAAGGAGG TTTCTCTACCAAG TACCCTAGAAGC TACCGAAGCAAG TACCTACCAAGA TTCCTCTACCAAG TACCCTACCAAGA TACCTACCAAGA TTCCTCTACCAAGA TACCTACCAAGA TTCTCTCTACCAAG TACCTACCAAGA TACCTACCAAGA TTCTCTACAAGA TTCTCTACAAGA TTCTCTACAAGA TACCTACCAAGA TACCTACCAAGA TACCTACACAAGA TACCTACACAAGA TACCTACACAAGA TACCTACACAAGA TACCTACAACAACAAACAACAACAACAACAACAACAACAA

GAICCIGGCG CGGCCCIGGC GIGCCIICII CAAGCIGCIG GCIGIGGIGC ICIICCICII CACCITIGGG CIGCIGCGGI GGAIIGACAA CITIGCCCAC AICICGGGGI ICAICAGIGG CCTCTTCCTC TCCTTCGCCT TCTTGCCCTA CATCAGCTTT GGCAAGTTCG ACCTGTACCG CTTCACTGAC AAGTTCTGTG AGAAGTACGA ACTGGACGCT CAGCTCCACA TCGATACGCG GAAACGCTGC CAGATCATCA TCTTTCAGGT GGTCTTCCTG GGCCTCCTGG CTGGCCTGGT GGICCICIIC TACGICTAIC CIGICCGCIG IGAGIGGIGI GAGIICCICA CCIGCAICCC TICGAAGCIT GCGGCCGCAC AGCIGIATAC ACGIGCAAGC CAGCCAGAAC ICGCICCIGA AGACCCAGAG GAICTCGAGC ACCACCACCA CCACCACTAA TGTTAATTAA GTIGGGCGTI GTAATCATAG TCATAATCAA TACTCCTGAC TGCGTTAGCA ATTTAACTGT GATAAACTAC CGCATTAAAG CTATTCGATG ATAAGCTGTC AAACATGATA ATTCTTGAAG ACGAAAGGGC CTAGGCTGAT AAAACAGAAT TTGCCTGGCG GCAGTAGCGC GGTGGTCCCA CCTGACCCCA TGCCGAACTC AGAAGTGAAA CGCCGTAGCG CCGATGGTAG TGTGGGGTCT CCCCATGCGA CGITITAICI GITGITIGIC GGIGAACGCI CICCIGAGIA GGACAAAICC GCCGGGAGCG GCCAGGCAIC AAATTAAGCA GAAGGCCAIC CIGACGGAIG GCCITITIGC GIITCIACAA GAGTAGGGAA CTGCCAGGCA TCAAATAAAA CGAAAGGCTC AGTCGAAAGA CTGGGCCTTT GATITIGAACG ITGCGAAGCA ACGGCCCGGA GGGTGGCGGG CAGGACGCCC GCCATAAACT ACTCTTTTGT TTATTTTTCT AAATACATTC AAATATGTAT CCGCTGAGCA ATAACTAGCA TAACCCCTIG GGGCCTCTAA ACGGGTCTTG AGGGGTTTTT TGCTGAAAGG AGGAACTATA TCCGGATTGG CGAATGGGAC GCGCCCTGTA GCGGCGCATT AAGCGCGGCG GGTGTGGTGG 1081 1141 1381 1441 1261 1321 1501 1561 1621 1741 1921 1681 1801 1861 1981 2041 2101 2161

TIACGCGCAG CGTGACCGCT ACACTTGCCA GCGCCCTAGC GCCCGCTCCT TTCGCTTTCT TCCCITCCIT ICTCGCCACG TTCGCCGGCT TTCCCCGTCA AGCTCTAAAT CGGGGGCTCC GATTAGGGTG CCACGITCII TAATAGIGGA CICTIGIICC AAACIGGAAC AACACICAAC CCIAICIGG TCTATTCTTT TGATTTATAA GGGATTTTGC CGATTTCGGC CTATTGGTTA AAAA1GAGC TGATTTAACA AAAATTTAAC GCGAATTTTA ACAAAATATT AACGTTTACA ATTTCTGGCG GCACGATGGC ATGAGATTAT CAAAAAGGAT CTTCACCTAG ATCCTTTTAA ATTAAAAATG ATGGTTCACG TAGTGGGCCA TCGCCCTGAT AGACGGTTTT TCGCCCTTTG ACGTTGGAGT AAGTTTTAAA TCAATCTAAA GTATATGA GTAAACTTGG TCTGACAGTT ACCAATGCTT AATCAGTGAG GCACCTATCT CAGCGATCTG TCTATTTCGT TCATCCATAG TTGCCTGACT CCCCGTCGTG TAGATAACTA CGATACGGGA GGGCTTACCA TCTGGCCCCA GTGCTGCAAT GATACCGCGA GACCCACGCT CACCGGCTCC AGAITTATCA GCAATAAACC AGCCAGCCGG AAGGGCCGAG CGCAGAAGIG GICCIGCAAC ITIAICCGCC ICCAICCAGI CIAITAAIIG TIGCCGGGAA GCTAGAGIAA GTAGIICGCC AGIIAAIAGI IIGCGCAACG IIGIIGCCAI TGCTACAGGC ATCGTGGTGT CACGCTCGTC GTTTGGTATG GCTTCATTCA GCTCCGGTTC TGGTTATGGC AGCACTGCAT AATICTCTTA CTGTCATGCC ATCCGTAAGA TGCTTTTCTG TGACTGGTGA TTAGCTCCTT GTACTCAACC AAGTCATICT GAGAATAGTG TAIGCGGCGA CCGAGTIGCI CTIGCCCGGC CCGATITIAGT GCTITIACGGC ACCTCGACCC CAAAAACTT CCAACGATCA AGGCGAGTTA CATGATCCCC CATGTTGTGC AAAAAAGCGG CGGTCCTCCG ATCGTTGTCA GAAGTAAGTT GGCCGCAGTG TTATCACTCA CTTTAGGGTT 2221 2341 2401 2461 2641 2521 2581 2701 2761 2821 2941 3001 3061 3181 3241 3301 3121

GTCAATACGG GATAATACCG CGCCACATAG CAGAACTTTA AAAGTGCTCA TCATTGGAAA GTTCGATGTA TTTCTGGGTG AGCAAAAACA GGAAGGCAAA ATGCCGCAAA AAAGGGAATA AGGGCGACAC GGAAATGTTG AATACTCATA CTCTTCCTTT TTCAATCATG ACCAAAATCC CTTAACGTGA GTTTTCGTTC CACTGAGCGT CAGACCCCGT AGAAAGATC AAAGGATCTT CTTGAGATCC TTTTTTTCTG TIGITIGCCG GATCAAGAGC TACCAACTCT TTTTCCGAAG GTAACTGGCT TCAGCAGAGC GCAGATACCA AATACTGTCC TTCTAGTGTA GCCGTAGTTA GGCCACCACT TCAAGAACTC TGTAGCACCG CCIACATACC ICGCICIGCI AAICCIGITA CCAGIGGCIG CIGCCAGIGG CGAIAAGICG TGTCTTACCG GGTTGGACTC AAGACGATAG TTACCGGATA AGGCGCAGCG GTCGGGCTGA ACGGGGGGTT CGTGCACACA GCCCAGCTTG GAGCGAACGA CCTACACCGA ACTGAGATAC CCGGTAAGCG GCAGGGTCGG AACAGGAGAG CGCACGAGGG AGCTTCCAGG GGGAAACGCC CTACAGCGTG AGCTATGAGA AAGCGCCACG CTTCCCGAAG GGAGAAAGGC GGACAGGTAT TGGTATCTTT ATAGTCCTGT CGGGTTTCGC CACCTCTGAC TTGAGCGTCG ATTTTTGTGA TGCTCGTCAG GGGGGGGAG CCTATGGAAA AACGCCAGCA ACGCGGCCTT TTTACGGTTC CIGGCCITII GCIGGCCIII IGCICACAIG IICIIIICCIG CGIIAICCCC IGAIICIGIG TTACCGCCTT TGAGTGAGCT GATACCGCTC GCCGCAGCCG AACGACCGAG CGCAGCGAGT CAGTGAGCGA GGAAGCCGGC GATAATGGCC TGCTTCTCGC CGAAACGTTT ACGITCTICG GGGCGAAAAC ICTCAAGGAI CITACCGCIG IIGAGAICCA TTCACCAGCG CGCGTAATCT GCTGCTTGCA AACAAAAAA CCACCGCTAC CAGCGGTGGT ACCCACTCGT GCACCCAACT GATCTTCAGC ATCTTTTACT GATAACCGTA 3361 3421 3481 3541 3601 3661 3721 3841 3961 4021 3901 4081 4141 4201 4261 4321 4381 4441

4501 GGTGGCGGGA CCAGTGACGA AGGCTTGAGC GAGGGCGTGC AAGATTCCGA ATACCGCAAG	4561 CGACAGGCCG ATCATCGTCG CGCTCCAGCG AAAGCGGTCC TCGCCGAAAA TGACCCAGAG	GTGCGGCGAC	CGAAAT
AAGATTCCGA	TCGCCGAAAA	ACAGTCATAA	TAACGICCCG
GAGGGCGTGC	AAAGCGGTCC	GATAAAGAAG	CGTGACATCA
AGGCTTGAGC	CGCTCCAGCG	CGAGTTGCAT	TCACAATTCT
CCAGTGACGA	ATCATCGTCG	ACCTGTCCTA	TTGTGAGCGC
GGTGGCGGGA	CGACAGGCCG	4621 CGCTGCCGGC ACCTGTCCTA CGAGTTGCAT GATAAAGAAG ACAGTCATAA GTGCGGCGAC	GACCGGTGAA TTGTGAGCGC TCACAATTCT CGTGACATCA TAACGTCCCG CGAAAT
4501	4561	4621	4681

Figure 52. HLA peptide motif search results

User Parameters and Scoring Information				
method selected to limit number of results	explicit number			
number of results requested	20			
HLA molecule type selected	A_0201			
length selected for subsequences to be scored	9			
echoing mode selected for input sequence	Y			
echoing format	numbered lines			
length of user's input peptide sequence	803			
number of subsequence scores calculated	795			
number of top-scoring subsequences reported back in scoring output table	20			

Scoring Results							
Rank	Start Position	Subsequence Residue Listing	Score (Estimate of Half Time of Disassociation of a Molecule Containing This Subsequence)				
1	425	MMPKYLNFV	1080.239				
2_	410	KLYVRRVFI	642.660				
3	557	RLLKKGYEV	257.342				
4	203	FLVADKVIV	131.175				
_5	144	LLHVTDTGV	118.238				
6	547	KEAESSPFV	106.738				
7	639 RLTESPCAL		87.586				
8	381 VTFKSILFV		76.863				
9	3 ALWVLGLCC		41.234				
10	6 VLGLCCVLL		36.316				
11	189 SELIGOFGV		29.023				
12	741	RMLRLSLNI	27.879				
13	451	TÖÖHKTTKA	27.573				
14	280	YVWSSKTET	24.895				
15	259	LELDTIKNL	24.638				
16	417	FITDDFHDM	24.478				
17	467	KTLDMIKKI	17.695				
18	463	KLVRKTLDM	17.388				

19	429	YLNFVKGVV	17.053
20	197	VGFYSAFLV	16.564

Figure 53. Suggested models for transmembrane topology for ICT1025

----> STRONGLY prefered model: N-terminus inside 2 strong transmembrane helices, total score: 2962 # from to length score orientation 1 3 19 (17) 2034 i-o 2 191 212 (22) 928 o-i

-----> alternative model
2 strong transmembrane helices, total score: 2607
# from to length score orientation
1 3 19 (17) 1929 o-i
2 191 213 (23) 678 i-o

Figure 54.."DAS" - Transmembrane Prediction server ICT 1025

Potential transmembrane seg	ements
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Start Stop I	ength-	~	Cutoff
6 18 1	3 -	~	1.7*
7 17 1	1.	~	2.2
195 209 1	5 -	~	1.7*
197 206 1	0 -	~	2.2
247 248 2		~	1.7
384 390 7	' -	~	1.7
710 723 1	4 ~	~	1.7
713 719 7	` ~	~	2.2*

## Living Cell surface ELISA for screening 1025-antibody containing supernatants in MDA-MB-435 cells

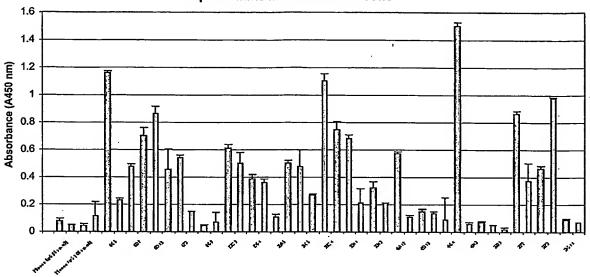


Figure 55. Screening of ICT1025 mAb for surface binding activities in breast tumor cell

The culture supernatants from 40 ICT1025 mAb secreting hybridoma clones were screened for the cell surface binding activities in MDA-MB-435 cells using a live cell surface staining ELISA assay. Mouse IgG at various concentration were used as non-specific controls. The clones with the highest cell surface binding activities (Absorbance value) were selected for mAb purification.

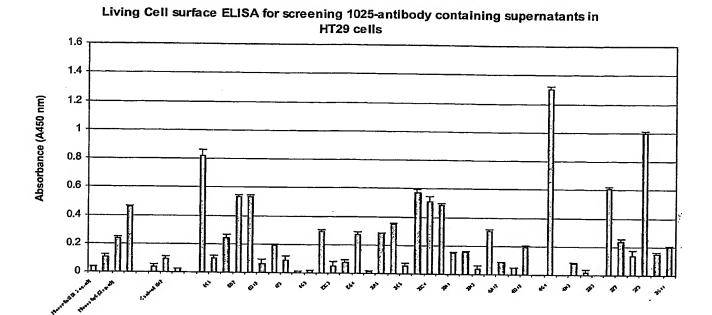
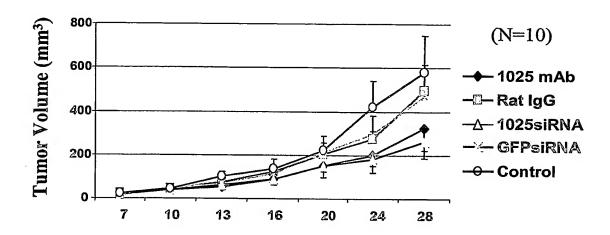


Figure 56. Screening of ICT1025 mAb for surface binding activities in colon tumor cells

The culture supernatants from 40 ICT1025 mAb secreting hybridoma clones were screened for the cell surface binding activities in HT29 cells using a live cell surface staining ELISA assay. Mouse IgG at various concentration were used as non-specific controls. Also, the supernatants from 3 GST mAb secreting hybridoma clones (2H2, 1H2, 3G3) were used as negative controls. The clones with the highest cell surface binding activities (Absorbance value) were selected for mAb purification.



## **Day Post Tumor Cell Inoculation**

Figure 57. Effect of inhibition of 1025 by antibody or siRNA on tumorigenesis and tumor growth. For antibody treatment, 5 million MDA-MB-435 cells were preincubated with 100 ug of 1025 mAb or Rat IgG in a total volume of 1ml culture medium at 37oC for 4 hours. After washing with PBS, the cells were inoculated into the Fat-pat of nude mice at 0.4 million cells per site. For siRNA treatment, 5 million MDA-MB-435 cells in were transfected with 10 ug of 1025 siRNA or GFP siRNA using electroporation, then cells were incubated in a total volume of 1ml culture medium at 37oC for 4 hours. After washing with PBS, the cells were inoculated into the Fat-pat of nude mice at 0.4 million cells per site. For control group, 5 million MDA-MB-435 cells were incubated in a total volume of 1ml culture medium at 37oC for 4 hours. After washing with PBS, the cells were inoculated into the Fat-pat of nude mice at 0.4 million cells per site.